

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 09:48:28 ; Search time 9333.87 seconds
(without alignments)
1181.073 Million cell updates/sec

Title: US-09-922-895-3

Perfect score: 3586

Sequence: 1 GATCCCTACCTTCCCATC.....CTATCAGGAGAACTGAA 3586

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hum:*

31: em_hum:*

32: em_hum:*

33: em_hum:*

34: em_hum:*

35: em_hum:*

36: em_hum:*

37: em_hum:*

38: em_hum:*

39: em_hum:*

40: em_hum:*

41: em_hum:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3586	100.0	3586	6	AR164120
2	3586	100.0	3586	6	AX030930
3	3494.4	97.4	5791	9	AF247361
4	3492.8	97.4	197279	9	AC104439
5	3481.6	97.1	220965	2	HSA31268
6	3408.6	95.1	7010	9	AF224496S2
7	3388	94.5	3388	9	AF237380S2
8	2406	67.1	7201	6	AX345239
9	2271.8	63.4	7201	6	AX345238
10	1066.2	29.7	1310	6	AF262300
11	358.6	10.0	436	9	AF262304
12	344.2	9.6	1915	6	BD006761
13	219.8	6.1	112967	9	AC025177
14	218.2	6.1	131329	9	AC004873
15	218.2	6.1	157435	9	HS30024
16	218.2	6.1	179517	2	AC026361
17	217.8	6.1	146740	9	CNS01D9X
18	217	6.1	151846	9	AP001630
19	217	6.1	180236	2	AC020600
20	217	6.1	255952	2	AL513473
21	217	6.1	340000	9	AP001748
22	216.6	6.0	39282	9	AC005596
23	215.6	6.0	120538	9	AC004815
24	215.6	6.0	121496	9	AC093391
25	215.2	6.0	45597	9	AP000533
26	215	6.0	174913	9	AL158819
27	214.8	6.0	93426	9	AL359732
28	214.6	6.0	38468	9	U51560
29	214.6	6.0	176343	9	CNS01D9X
30	214.4	6.0	185376	9	AC005096
31	213.6	6.0	56913	9	HS67C13
32	212.8	5.9	124950	9	AC108059
33	212.8	5.9	136876	9	AC112499
34	212.8	5.9	177957	2	AC025298
35	212.6	5.9	37650	9	HSU31B10
36	212.6	5.9	123708	9	HS1190A9
37	212.6	5.9	145656	9	HS11K10
38	212.6	5.9	340090	9	HS21C009
39	212.4	5.9	109445	9	AC008946
40	212.4	5.9	134184	9	AC095044
41	212.4	5.9	215705	9	AL589931
42	212.4	5.9	241257	9	AC022146
43	212.2	5.9	135144	2	AC093248
44	212.2	5.9	185332	9	AC016673
45	212.2	5.9	224931	9	AC008540

ALIGNMENTS

RESULT 1

LOCUS AR164120

DEFINITION Sequence 3 from patent US 6271347.

ACCESSION AR164120

VERSION AR164120.1 GI:16235066

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3586)

AUTHORS Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.

TITLE Biotinophil eotaxin receptor

JOURNAL Patent: US 6271347-A 3 07-AUG-2001.

FEATURES Location/Qualifiers

```
source 1. .3586 /organism="unknown"
BASE COUNT 1003 a 784 c 701 g 1098 t
ORIGIN
Query Match 100.0%; Score 3586; DB 6; Length 3586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCCCTACCTTCCCATCAGACTAGGGGGCATGGAGGCGCTCTGCTAGATGGGGA 60
DB 1 GGATCCCTACCTTCCCATCAGACTAGGGGGCATGGAGGCGCTCTGCTAGATGGGGA 60
QY 61 CCCCCAAGAATGTCTCCCTGTGGGCACTCTTACCAGATGGGATGGCCAGCGGTT 120
DB 61 CCCCCAAGAATGTCTCCCTGTGGGCACTCTTACCAGATGGGATGGCCAGCGGTT 120
QY 121 AAGTGTGTGTGACGAGCAAAAAAAGATCTAGTTTGTACTCTTGAGAGTTCTCGGTTT 180
DB 121 AAGTGTGTGTGACGAGCAAAAAAAGATCTAGTTTGTACTCTTGAGAGTTCTCGGTTT 180
QY 181 GTTCATGGCATGGGCGAGGAGTCAAGGAGCAGCCTTGCCTCAGTCCCTACCAAGTCA 240
DB 181 GTTCATGGCATGGGCGAGGAGTCAAGGAGCAGCCTTGCCTCAGTCCCTACCAAGTCA 240
QY 241 GGAAGAAGTGCATAGCCTGGGCGCAGGGCCAGGCGCTGTGTGAGGCGTAGTGTAACGA 300
DB 241 GGAAGAAGTGCATAGCCTGGGCGCAGGGCCAGGCGCTGTGTGAGGCGTAGTGTAACGA 300
QY 301 GAGGGCTCTCCATTCCTCCAGCCCAAGGAAGACTAAGATGATACTCATGAGTATTTAGC 360
DB 301 GAGGGCTCTCCATTCCTCCAGCCCAAGGAAGACTAAGATGATACTCATGAGTATTTAGC 360
QY 361 TACAACACACACAGCAGGTTCCAGAAAAAGGCTCAGGCTTGGAAACAGGTCAACCCAC 420
DB 361 TACAACACACACAGCAGGTTCCAGAAAAAGGCTCAGGCTTGGAAACAGGTCAACCCAC 420
QY 421 TCACAGACACACAGCTCATATTAATCAAGAGCAACAGAGAGCAGGAACACCCCTTCCA 480
DB 421 TCACAGACACACAGCTCATATTAATCAAGAGCAACAGAGAGCAGGAACACCCCTTCCA 480
QY 481 CTCTGCCCATGTCTCAAGTTGTAGTGGCCCTCCCTCAGATCTCTGCGCACACTTAGA 540
DB 481 CTCTGCCCATGTCTCAAGTTGTAGTGGCCCTCCCTCAGATCTCTGCGCACACTTAGA 540
QY 541 AAGGAACACACAGGAAAGAACTGAATTAATTAAGCTGACAGCATAAAGAGATAGTAAA 600
DB 541 AAGGAACACACAGGAAAGAACTGAATTAATTAAGCTGACAGCATAAAGAGATAGTAAA 600
QY 601 ACCTAAATCATTTGTTCACATGAATGAATCAAGAAATTTAAACCACTTTGACTAAA 660
DB 601 ACCTAAATCATTTGTTCACATGAATGAATCAAGAAATTTAAACCACTTTGACTAAA 660
QY 661 TGTGTGATCTTTTCTCTGATCCAGCAGATAGAAAGCTGGTAACAGAGACACATA 720
DB 661 TGTGTGATCTTTTCTCTGATCCAGCAGATAGAAAGCTGGTAACAGAGACACATA 720
QY 721 GTTTGAGACTAAAGATCATTTGCACATTTCACTGCTGAGTGTATTTGTGATTTTA 780
DB 721 GTTTGAGACTAAAGATCATTTGCACATTTCACTGCTGAGTGTATTTGTGATTTTA 780
QY 781 GTTGACCTCACTTTGTAATCTTGACACAGGGGCAATCCAATATCTGCACAAAGATATG 840
DB 781 GTTGACCTCACTTTGTAATCTTGACACAGGGGCAATCCAATATCTGCACAAAGATATG 840
QY 841 TTAAACAGTGTAAATCTGATGAGAGAGATTTGATTTTACTTTCTTTTGTGCT 900
DB 841 TTAAACAGTGTAAATCTGATGAGAGATTTGATTTTACTTTCTTTTGTGCT 900
QY 901 CTCTCTTCTATTTGTCTTACTTATTTACGATTTACCTATCGTTTCCCAAAATGTAAAA 960
DB 901 CTCTCTTCTATTTGTCTTACTTATTTACGATTTACCTATCGTTTCCCAAAATGTAAAA 960
```

```
QY 961 GGCCATTTTGAAGCCCAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTTG 1020
DB 961 GGCCATTTTGAAGCCCAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTTG 1020
QY 1021 ATTGAGACTGGGTAAGACAGGTGAAGAACCATATCAGGTTTTTAATTTTAAATTTTAA 1080
DB 1021 ATTGAGACTGGGTAAGACAGGTGAAGAACCATATCAGGTTTTTAATTTTAAATTTTAA 1080
QY 1081 ATTTATTTATTTATTTATTTTGTAGATGAGATGAGTGTGCTGCGCCAGGCTGGAGTGCAG 1140
DB 1081 ATTTATTTATTTATTTATTTTGTAGATGAGTGTGCTGCGCCAGGCTGGAGTGCAG 1140
QY 1141 CGGCGTATCACAGTTCACGACCTCAACCTTCTAGGCTCAAGGATTTCCACACTC 1200
DB 1141 CGGCGTATCACAGTTCACGACCTCAACCTTCTAGGCTCAAGGATTTCCACACTC 1200
QY 1201 AGCCCCCAAGTAGTTGGGACACACAGTATGCGCCACATGCTGAGCTAAATTTCTAATTT 1260
DB 1201 AGCCCCCAAGTAGTTGGGACACACAGTATGCGCCACATGCTGAGCTAAATTTCTAATTT 1260
QY 1261 TTTTGTAGAGATNGAGTCACTATATTTGCCAGGCTGTGTGAATTTCTGGGCTCAGG 1320
DB 1261 TTTTGTAGAGATNGAGTCACTATATTTGCCAGGCTGTGTGAATTTCTGGGCTCAGG 1320
QY 1321 TGAGCTTCCACACTGGGCTCCCAAGTAGTGGGATTAAGAGCATAGGATGCTCCCT 1380
DB 1321 TGAGCTTCCACACTGGGCTCCCAAGTAGTGGGATTAAGAGCATAGGATGCTCCCT 1380
QY 1381 GCCCATATGAGATTTTGTCTGTGATCCATGACGTAGTAAATCAAGACTTGGCTGT 1440
DB 1381 GCCCATATGAGATTTTGTCTGTGATCCATGACGTAGTAAATCAAGACTTGGCTGT 1440
QY 1441 GACTCTGAGAGACCTGCATGCTTCTGAGCTGGAATCTCAGTCAAGGATCAAGGATAGG 1500
DB 1441 GACTCTGAGAGACCTGCATGCTTCTGAGCTGGAATCTCAGTCAAGGATCAAGGATAGG 1500
QY 1501 CAGCCCTGAAAACCCAAACCAAAAGTTCTATGTTATCATCTCGATCATGTTGATTTA 1560
DB 1501 CAGCCCTGAAAACCCAAACCAAAAGTTCTATGTTATCATCTCGATCATGTTGATTTA 1560
QY 1561 TAGAAATTAACACATGATTTAAAGACACTACCTCAAACTGAGCAAACTTAAGTAATTTT 1620
DB 1561 TAGAAATTAACACATGATTTAAAGACACTACCTCAAACTGAGCAAACTTAAGTAATTTT 1620
QY 1621 TTTAAATTTGACCTGTTTTTAAATCACTCTGGAGAAAAGAAAATTAATACAAATA 1680
DB 1621 TTTAAATTTGACCTGTTTTTAAATCACTCTGGAGAAAAGAAAATTAATACAAATA 1680
QY 1681 TTAAGGTGAATACAGGCTACTATACCTTGTCTCCAGATTAAGCAGTTCTGTTCTTT 1740
DB 1681 TTAAGGTGAATACAGGCTACTATACCTTGTCTCCAGATTAAGCAGTTCTGTTCTTT 1740
QY 1741 CTTCGCTTTAATGCTGAAGTGCAGAAAGACACATCTGTGATTTGACGTGTAACTGCAA 1800
DB 1741 CTTCGCTTTAATGCTGAAGTGCAGAAAGACACATCTGTGATTTGACGTGTAACTGCAA 1800
QY 1801 AATGTATTTTCTCTCAAGCTCTATGAGTTGAGTTATGATTAATTAAGATGTC 1860
DB 1801 AATGTATTTTCTCTCAAGCTCTATGAGTTGAGTTATGATTAATTAAGATGTC 1860
QY 1861 TGATGGAGACACACAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGCCTGGA 1920
DB 1861 TGATGGAGACACACAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGCCTGGA 1920
QY 1921 ATGTGCAATTTGATCAGTGGAGATGTACTGTGACAGCCATGAAAAGACATCAACAGT 1980
DB 1921 ATGTGCAATTTGATCAGTGGAGATGTACTGTGACAGCCATGAAAAGACATCAACAGT 1980
QY 1981 TCCACCCAAAGGACCCATTTTCTCAATTTCAATTTGAATGGCTTATATGCTCTCT 2040
DB 1981 TCCACCCAAAGGACCCATTTTCTCAATTTCAATTTGAATGGCTTATATGCTCTCT 2040
QY 2041 TTCAATCTGCTTCTTACAGATTTTACAGCTTTTCTGTGTTCAAAATGTGACTCACATA 2100
```

```
|||||
Db 2041 TTCAATCCGCTCCACAGTTTACAGCTTTTCTGTTCAAAATGTAACACACATA 2100
OY 2101 CACTCATTTTCCATCACACACCCCAAGTACCCATTTGGCCCTTCATGATATA 2160
Db 2101 CACTCATTTTCCATCACACACCCCAAGTACCCAAATGGCTCCACTTTTGATATA 2160
OY 2161 GTAAAGAGGCTCTGCATTAAAGGGCTTGTCAAGCAGCAGCTGAGAGCGCTAGACT 2220
Db 2161 GTAAAGAGGCTCTGCATTAAAGGGCTTGTCAAGCAGCAGCTGAGAGCGCTAGACT 2220
OY 2221 GGCTCATTTCCATCTCTATTTCTCACTGACTTGAATCCCAAGAACCATGTGGG 2280
Db 2221 GGCTCATTTCCATCTCTATTTCTCACTGACTTGAATCCCAAGAACCATGTGGG 2280
OY 2281 CCTCAGTATTCGATCAATTAATCTATTAGAAGCAAAAACAAATCCCGCATTTGGCCCA 2340
Db 2281 CCTCAGTATTCGATCAATTAATCTATTAGAAGCAAAAACAAATCCCGCATTTGGCCCA 2340
OY 2341 GTTATTAAACATTTCTCAGATTTCCTTGAGAATGCCCCATCGGCTGTATTTACATC 2400
Db 2341 GTTATTAAACATTTCTCAGATTTCCTTGAGAATGCCCCATCGGCTGTATTTACATC 2400
OY 2401 TTTCACCTTTGCTCCCTTCCTCTAGAAAAGAAAGTCAAGTTGGATGCCCTTGAGAACT 2460
Db 2401 TTTCACCTTTGCTCCCTTCCTCTAGAAAAGAAAGTCAAGTTGGATGCCCTTGAGAACT 2460
OY 2461 AGTGCATGGCTTACGTGCTTCCATGACTCCGCTTATCTGTCTTTCTATTTTCTCTCT 2520
Db 2461 AGTGCATGGCTTACGTGCTTCCATGACTCCGCTTATCTGTCTTTCTATTTTCTCTCT 2520
OY 2521 TTTCACCGCAAGTCTATTAATCTCAGAAAAAGCAGCAGCTGGCTTGGGCTCTGGCTTA 2580
Db 2521 TTTCACCGCAAGTCTATTAATCTCAGAAAAAGCAGCAGCTGGCTTGGGCTCTGGCTTA 2580
OY 2581 AGAAATATCAAGTCCAGTGAAGAAATCCATGTGACGACCCCTCTGCTTACCCTTTGTTG 2640
Db 2581 AGAAATATCAAGTCCAGTGAAGAAATCCATGTGACGACCCCTCTGCTTACCCTTTGTTG 2640
OY 2641 ATGAGAACGCTCCAGGGGTTGCTTTTGCATGTTACAGAGGCTTAACAGATACCA 2700
Db 2641 ATGAGAACGCTCCAGGGGTTGCTTTTGCATGTTACAGAGGCTTAACAGATACCA 2700
OY 2701 GGGGCAAGAAAGAAAGTAACCTTAACATAATGCTCTTATTAATTTGTAATTA 2760
Db 2701 GGGGCAAGAAAGAAAGTAACCTTAACATAATGCTCTTATTAATTTGTAATTA 2760
OY 2761 GTTAATTTACTGTGATTTGTACATGTGTACAGACAAATGTGATTTTTTTCACAGCTGCT 2820
Db 2761 GTTAATTTACTGTGATTTGTACATGTGTACAGACAAATGTGATTTTTTTCACAGCTGCT 2820
OY 2821 GTGATTTGGATTATGCAATTTTGAATGAAGATCTGTAAAGACACACAAGGATGCC 2880
Db 2821 GTGATTTGGATTATGCAATTTTGAATGAAGATCTGTAAAGACACACAAGGATGCC 2880
OY 2881 TCAGAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAAAATCACTCAATTTGAATCTAGT 2940
Db 2881 TCAGAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAAAATCACTCAATTTGAATCTAGT 2940
OY 2941 GACAGAGAAATGGACATGGATAGACATTAAGATCTAGCCCAATTTTATATTTACTTTC 3000
Db 2941 GACAGAGAAATGGACATGGATAGACATTAAGATCTAGCCCAATTTTATATTTACTTTC 3000
OY 3001 TTGAGAGATTTTGAACAAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAACATA 3060
Db 3001 TTGAGAGATTTTGAACAAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAACATA 3060
OY 3061 ATGAATGTCTCATCATTAAGGGCCCTGAGAAAGCATTAATTTACTTTGTAATTTGTAATATC 3120
Db 3061 ATGAATGTCTCATCATTAAGGGCCCTGAGAAAGCATTAATTTACTTTGTAATTTGTAATATC 3120
OY 3121 ATGTGTTATTTATTTATACATATTTTGTCTTTTAAATGATTAAGGATTTTAAAGGTATATG 3180
|||||
```

```
Db 3121 ATGTGTTATTTATTTATTTATTTATTTGCTTTTAAATGATTAAGGATTTTAAAGGTATATG 3180
OY 3181 TAAACGTAAACATTAATAATGCAAAATGCGGTAGAGACAGTAGTAATAATATGATAT 3240
Db 3181 TAAACGTAAACATTAATAATGCAAAATGCGGTAGAGACAGTAGTAATAATATGATAT 3240
OY 3241 TATATTTGTTATCATTAATTTAGCTGTTTTTCTGTTGTTGTTATTTCTTTAAATGCT 3300
Db 3241 TATATTTGTTATCATTAATTTAGCTGTTTTTCTGTTGTTGTTATTTCTTTAAATGCT 3300
OY 3301 TACAGAAATCTGTATCTCCATTTCTTACACACACCCCAACAATTTCTGCTTTTCCC 3360
Db 3301 TACAGAAATCTGTATCTCCATTTCTTACACACACCCCAACAATTTCTGCTTTTCCC 3360
OY 3361 ATGCCGGTATGCTTACCTTTGAAGAGCTTGAAGCTTCTCTCTCAATCTCTCTGCG 3420
Db 3361 ATGCCGGTATGCTTACCTTTGAAGAGCTTGAAGAGCTTCTCTCTCAATCTCTCTGCG 3420
OY 3421 ACCTTGATATGCTTTTGAATTCATGTTAAAGAAATCCCTAGGCTTACATCATGATGG 3480
Db 3421 ACCTTGATATGCTTTTGAATTCATGTTAAAGAAATCCCTAGGCTTACATCATGATGG 3480
OY 3481 CATCTTTGTTGATGATCATGATTAATCAACGTGTGTTTACGAAGATGATTAATGCTT 3540
Db 3481 CATCTTTGTTGATGATCATGATTAATCAACGTGTGTTTACGAAGATGATTAATGCTT 3540
OY 3541 CATTTGGGATGTTATTTTCTCTCTCTATACAGGAGAGAGGAA 3586
Db 3541 CATTTGGGATGTTATTTTCTCTCTCTATACAGGAGAGAGGAA 3586

RESULT 2
AX030930
LOCUS AX030930 3586 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 3 from Patent EP1012190.
ACCESSION AX030930
VERSION AX030930.1 GI:10278335
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE
1 (bases 1 to 3586)
AUTHORS Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.
TITLE Eosinophil eotaxin receptor
JOURNAL Patent: EP 1012190-A 3 28-JUN-2000;
MERCK & CO INC (US)
FEATURES
location/Qualifiers
source
1..3586
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 1003 a 784 c 701 g 1098 t
ORIGIN
Query Match 100.0%; Score 3586; DB 6; Length 3586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGAATCCCTACCTCCCATCAGAGCTAAGGGGAGTGAAGGCGCTGCTGAAGATGGGA 60
Db 1 GGAATCCCTACCTCCCATCAGAGCTAAGGGGAGTGAAGGCGCTGCTGAAGATGGGA 60
OY 61 CCCCAGAAGATGTCCTCGTGGGACACTTCTTACAGATGGATGGCAGTGGGTT 120
Db 61 CCCCAGAAGATGTCCTCGTGGGACACTTCTTACAGATGGATGGCAGTGGGTT 120
OY 121 AAGTGGTGTCAGGAGAAAAAAGATCTAGTTTGTACTCTTGAAGTTCCTGCGTTT 180
Db 121 AAGTGGTGTCAGGAGAAAAAAGATCTAGTTTGTACTCTTGAAGTTCCTGCGTTT 180
OY 181 GTTCATGGCATGGGACAGGAGTCAAGAGCAGACGCTTGCCATGCTTACCATGCA 240
Db 181 GTTCATGGCATGGGACAGGAGTCAAGAGCAGACGCTTGCCATGCTTACCATGCA 240
OY 181 GTTCATGGCATGGGACAGGAGTCAAGAGCAGACGCTTGCCATGCTTACCATGCA 240
|||||
```

QY	241	GGAAAAGTGATAGCTGGGGCCAGGGCCAGGGCCCTGGTGGAGGCGTAGTGTGTAACGA	300
Db	241	GGAAAAGTGATAGCTGGGGCCAGGGCCAGGGCCCTGGTGGAGGCGTAGTGTGTAACGA	300
QY	301	GAGGGCTCTCCATTCGAGGCCCAAGGAAGATAGATGAAATCCATGATAGATATTAGC	360
Db	301	GAGGGCTCTCCATTCGAGGCCCAAGGAAGATAGATGAAATCCATGATAGATATTAGC	360
QY	361	TACAAACCCACACGACGAGTTCCAGAAAAAGGCTCAGCCTTGGAAACAGGTACCCCCAC	420
Db	361	TACAAACCCACACGACGAGTTCCAGAAAAAGGCTCAGCCTTGGAAACAGGTACCCCCAC	420
QY	421	TCAGCAGACACCACTCATATTAATCAAGACCCACACAGGAGACAGAACACCCCTTCCCA	480
Db	421	TCAGCAGACACCACTCATATTAATCAAGACCCACACAGGAGACAGAACACCCCTTCCCA	480
QY	481	CTCTCCCCCATGTCTCAAGTTGTGTGGCCCTTCACAGATCTCTGCCACCATTTTGA	540
Db	481	CTCTCCCCCATGTCTCAAGTTGTGTGGCCCTTCCTCCAGATCTCTGCCACCATTTTGA	540
QY	541	AAGGACACTGAAGAAGAAACTGAAATTATTAAGCTGACAGCATAAAGAGATGAGTAAA	600
Db	541	AAGGACACTGAAGAAGAAACTGAAATTATTAAGCTGACAGCATAAAGAGATGAGTAAA	600
QY	601	ACCTAAATTCATTTCTCAGATGATGATTAAGAGAAGTTTAAACCACTTGGACTAAA	660
Db	601	ACCTAAATTCATTTCTCAGATGATGATTAAGAGAAGTTTAAACCACTTGGACTAAA	660
QY	661	TGTGTGAATCCCTTTTCTCGTATCCAGAGATGAAGACGTGGTAAACAGACCAACATA	720
Db	661	TGTGTGAATCCCTTTTCTCGTATCCAGAGATGAAGACGTGGTAAACAGACCAACATA	720
QY	721	GTTTGGAGACTAAAGAAATCATATGACATTTCACTGCTGAGTGTATGTGAGTAATTTTA	780
Db	721	GTTTGGAGACTAAAGAAATCATATGACATTTCACTGCTGAGTGTATGTGAGTAATTTTA	780
QY	781	GTTGACCCCACTTTGTATAATCTTGACACAGGGGCATCCAAATCTGCACAAAGATATG	840
Db	781	GTTGACCCCACTTTGTATAATCTTGACACAGGGGCATCCAAATCTGCACAAAGATATG	840
QY	841	TTAACCACTGTAAATCTGCATGAGAGATTGGGTGATTTTACTTGGTTTGTGCT	900
Db	841	TTAACCACTGTAAATCTGCATGAGAGATTGGGTGATTTTACTTGGTTTGTGCT	900
QY	901	CTTCTTCTTATTTGTCTTACTTAATTTAGATTAACCATACCTATCGTTTTCCCAAAATGTA	960
Db	901	CTTCTTCTTATTTGTCTTACTTAATTTAGATTAACCATACCTATCGTTTTCCCAAAATGTA	960
QY	961	GGCCATTTTGAACCCCTTAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTTG	1020
Db	961	GGCCATTTTGAACCCCTTAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTTG	1020
QY	1021	ATTGACCTGGGTGACAGAGGGAAGAACCATATCAGGTTTATATTTTAAATTTTAAT	1080
Db	1021	ATTGACCTGGGTGACAGAGGGAAGAACCATATCAGGTTTATATTTTAAATTTTAAAT	1080
QY	1081	ATTATTTTATTTATTTATTTTGGATGAGAGTCTGGCTGCGCCAGGCTGAGAGTCAG	1140
Db	1081	ATTATTTTATTTATTTATTTTGGATGAGAGTCTGGCTGCGCCAGGCTGAGAGTCAG	1140
QY	1141	CGGCGTATCACAAGTCTACATGACAGCTTCAACCTTTTAAAGGATTTCCCAACCTC	1200
Db	1141	CGGCGTATCACAAGTCTACATGACAGCTTCAACCTTTTAAAGGATTTCCCAACCTC	1200
QY	1201	AGCCCCCAAGTATGATGGGAACACAGCTATGAGGCGCAACATGGCTGGCTAATTTCTATTT	1260
Db	1201	AGCCCCCAAGTATGATGGGAACACAGCTATGAGGCGCAACATGGCTGGCTAATTTCTATTT	1260
QY	1261	TTTTTTAGAGATAGATCTCACTATATTTGCACAGGCTGGCTTGAATTTCTGGGCTCAGG	1320
Db	1261	TTTTTTAGAGATAGATCTCACTATATTTGCACAGGCTGGCTTGAATTTCTGGGCTCAGG	1320
QY	1321	TGAGGCTCCACCTGGGCTTCCCAAGATCTGGGATTTACAGGCAATGACCAAGTCCCT	1380

Dp	1321	TCAGCCCTCCACCGGGCCCTCCCAAAATCATGGGATTAAGGACATGAGCAAGGTCCT	1380
Qy	1381	GCCCATATGAAATTTCTGCTCGTGATGCCATGCACCTAGTATCAAGACTGGCTCT	1440
Dp	1381	GCCCATATGAAATTTCTGCTCGTGATGCCATGCACCTAGTATCAAGACTGGCTCT	1440
Qy	1441	GACTCTGGAGGACCTGCATGCTTCTTGGAGCTTGAACTTCAGTGCCTAAAGCTCATAG	1500
Dp	1441	GACTCTGGAGGACCTGCATGCTTCTTGGAGCTTGAACTTCAGTGCCTAAAGCTCATAG	1500
Qy	1501	CAGCCCTGAAAACCCAAACCAAAAGGTTCTATGCTTATCATCTGATCATGTGATTTTA	1560
Dp	1501	CAGCCCTGAAAACCCAAACCAAAAGGTTCTATGCTTATCATCTGATCATGTGATTTTA	1560
Qy	1561	TAGAAATTAACATGAAATTTAAAGACATACCCCTCAACAGGAGCAAAACCTTAAGTAA	1620
Dp	1561	TAGAAATTAACATGAAATTTAAAGACATACCCCTCAACAGGAGCAAAACCTTAAGTAA	1620
Qy	1621	TTTAAAGTTTGACCTGTTTTTAAATCATCTCTTGAGAAAAAGAAATTAATACAAATA	1680
Dp	1621	TTTAAAGTTTGACCTGTTTTTAAATCATCTCTTGAGAAAAAGAAATTAATACAAATA	1680
Qy	1681	TTTAAGGGATTAACAGCTACTATACCTTGTCTCCAGATTTAGACATGTCGTTCTTTT	1740
Dp	1681	TTTAAGGGATTAACAGCTACTATACCTTGTCTCCAGATTTAGACATGTCGTTCTTTT	1740
Qy	1741	CTTGCTTTAGATGCTGGAAGTGCAGAAAGACATCTGTGATTTAGCTGTTAACTGACAA	1800
Dp	1741	CTTGCTTTAGATGCTGGAAGTGCAGAAAGACATCTGTGATTTAGCTGTTAACTGACAA	1800
Qy	1801	AATGTATATTTTTTCTCAGCTGCTATGAGATTGATATGCTATTTAGATTAAGATATGC	1860
Dp	1801	AATGTATATTTTTTCTCAGCTGCTATGAGATTGATATGCTATTTAGATTAAGATATGC	1860
Qy	1861	TGATGGGAGACACACAACCAATTTGTTCTCAGTGCATTTTCTCTCAAAAGCCTGGA	1920
Dp	1861	TGATGGGAGACACACAACCAATTTGTTCTCAGTGCATTTTCTCTCAAAAGCCTGGA	1920
Qy	1921	ATGTGCCATTTATCAGTGGGAGATGTCTCGACACACACCATGAAAGAGATCAACAAGT	1980
Dp	1921	ATGTGCCATTTATCAGTGGGAGATGTCTCGACACACACCATGAAAGAGATCAACAAGT	1980
Qy	1981	TCACCCCAAGGAGACCTATTTTTCTATTTTCTATTTGAATGGCTTCTATATGTCCTCT	2040
Dp	1981	TCACCCCAAGGAGACCTATTTTTCTATTTTCTATTTGAATGGCTTCTATATGTCCTCT	2040
Qy	2041	TTTCATTTCTGCTTCTACAGATTTTACAGCTTTTCTGGTTCAATGTGAACCTACATA	2100
Dp	2041	TTTCATTTCTGCTTCTACAGATTTTACAGCTTTTCTGGTTCAATGTGAACCTACATA	2100
Qy	2101	CACCTCATTTTTCTCTATCACAACCCCAAGTAGTACCCTATGCTCTCATTTCCATATATA	2160
Dp	2101	CACCTCATTTTTCTCTATCACAACCCCAAGTAGTACCCTATGCTCTCATTTCCATATATA	2160
Qy	2161	GTAAGAAGAGGCTGTGCATTTAAGGGCTTGTCCAAGGACGACGCTGAGAGGCTAGACT	2220
Dp	2161	GTAAGAAGAGGCTGTGCATTTAAGGGCTTGTCCAAGGACGACGCTGAGAGGCTAGACT	2220
Qy	2221	GGCTCCATTTCCATCTCTATTTCTACAGCTTTGACTACCCAGAACCACATGTGGGG	2280
Dp	2221	GGCTCCATTTCCATCTCTATTTCTACAGCTTTGACTACCCAGAACCACATGTGGGG	2280
Qy	2281	CCTGAGTTTCAGTCAATTTATTCATTTAAGACCAAAACAAATTCGCCGATTTGGCCCCA	2340
Dp	2281	CCTGAGTTTCAGTCAATTTATTCATTTAAGACCAAAACAAATTCGCCGATTTGGCCCCA	2340
Qy	2341	GTTATTAAAGCAATTTCTCAGATTTACCTTGAAGAAATCCATGGGCTGTATTTACATC	2400
Dp	2341	GTTATTAAAGCAATTTCTCAGATTTACCTTGAAGAAATCCATGGGCTGTATTTACATC	2400
Qy	2401	TTACACCTTTGTCCTCTCTCAGAAAGAAAGTCACTTGGATGCCCCCTGAGGAAT	2460
Dp	2401	TTACACCTTTGTCCTCTCTCAGAAAGAAAGTCACTTGGATGCCCCCTGAGGAAT	2460

Db 2401 TTCACCCCTTGCCCTTCCCTCCTAGAAAAGAGAAAGTCACTGGATGCCCCCTGAGAGACT 2460
Oy 2461 AGTGCATGGCTTAAGTGTCTCCATGACTCCGCTTATGTTTTCTATTTCTCTCT 2520
Db 2461 AGTGCATGGCTTAAGTGTCTCCATGACTCCGCTTATGTTTTCTATTTCTCTCT 2520
Oy 2521 TTTTCACCGCAAGCTTAATATCTCAAGAAAAGCAGGCACTGGCTTAGGGCTCCTGGCCTA 2580
Db 2521 TTTTCACCGCAAGCTTAATATCTCAAGAAAAGCAGGCACTGGCTTAGGGCTCCTGGCCTA 2580
Oy 2581 AAAAAATATCAAGTCCAGTGAAGAAATCCCATGACGACCCCTCCCTGATACCCCTTTGTG 2640
Db 2581 AAAAAATATCAAGTCCAGTGAAGAAATCCCATGACGACCCCTCCCTGATACCCCTTTGTG 2640
Oy 2641 ATGGAGAAGCTCCCAAGGGGTTGCTTTTGCATGTTACAGGCGCTACACAGATCACA 2700
Db 2641 ATGGAGAAGCTCCCAAGGGGTTGCTTTTGCATGTTACAGGCGCTACACAGATCACA 2700
Oy 2701 GGGGCAAGAAAAGAAAGTAACCTAACTAATGCTTATATTTGTAATTTATTTGTAATA 2760
Db 2701 GGGGCAAGAAAAGAAAGTAACCTAACTAATGCTTATATTTGTAATTTATTTGTAATA 2760
Oy 2761 GTTAAATTAAGTGTATGATGTGTACAGACAAAATGTAATTTTTCACAGCTGCT 2820
Db 2761 GTTAAATTAAGTGTATGATGTGTACAGACAAAATGTAATTTTTCACAGCTGCT 2820
Oy 2821 GTGATTTGATTAATGCAATTTGGAATTAAGATGCTTTAAGACACACAAGCAGGTTCC 2880
Db 2821 GTGATTTGATTAATGCAATTTGGAATTAAGATGCTTTAAGACACACAAGCAGGTTCC 2880
Oy 2881 TCAAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATCATCAATTTGAACTAGT 2940
Db 2881 TCAAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATCATCAATTTGAACTAGT 2940
Oy 2941 GACAGAGAAAAGGAGCATGATAGAGACTAAGATCTACCCCAATTTATTTACTTG 3000
Db 2941 GACAGAGAAAAGGAGCATGATAGAGACTAAGATCTACCCCAATTTATTTACTTG 3000
Oy 3001 TTAGAGATTTTGAACAATTAATTAATTTCTCAAGTTCAATTTCCCATTAATCTATA 3060
Db 3001 TTAGAGATTTTGAACAATTAATTAATTTCTCAAGTTCAATTTCCCATTAATCTATA 3060
Oy 3061 ATGAATGTCTCATTAATTTAGGGCCCTGGAGAGACATAATTAATTTGTAATTAATC 3120
Db 3061 ATGAATGTCTCATTAATTTAGGGCCCTGGAGAGACATAATTAATTTGTAATTAATC 3120
Oy 3121 ATTTGTAATTAATTTATTAATTTGCTTTTAAATGATAGGATTTTAAAGTATAG 3180
Db 3121 ATTTGTAATTAATTTATTAATTTGCTTTTAAATGATAGGATTTTAAAGTATAG 3180
Oy 3181 TAAACTGTAAACATTAATTAATTAATTTGCTTTTAAATGATAGGATTTTAAATGAT 3240
Db 3181 TAAACTGTAAACATTAATTAATTAATTTGCTTTTAAATGATAGGATTTTAAATGAT 3240
Oy 3241 TAAATTTGTAATTAATTTAGGCTTTTCTGTTGTAATTTCTCTTTAAATGCT 3300
Db 3241 TAAATTTGTAATTAATTTAGGCTTTTCTGTTGTAATTTCTCTTTAAATGCT 3300
Oy 3301 TACAGAAATCTGATCCCATTTCTACACACACCCACACACTTTGCTTTTCCC 3360
Db 3301 TACAGAAATCTGATCCCATTTCTACACACACCCACACACTTTGCTTTTCCC 3360
Oy 3361 ATGCCGATATGCTTAATTTGAAGAGTCTTCTCTCTCTCAATCCTTCTCTGCTG 3420
Db 3361 ATGCCGATATGCTTAATTTGAAGAGTCTTCTCTCTCTCAATCCTTCTCTGCTG 3420
Oy 3421 ACCCTGATATGCTTTGAAATTCATGTTAAAGAAATCCCTAGGCTGATACATGCTG 3480
Db 3421 ACCCTGATATGCTTTGAAATTCATGTTAAAGAAATCCCTAGGCTGATACATGCTG 3480
Oy 3481 CATCTTTGTTGATACATGAATTAATCAACTGCTGTTTACGAAGGATGATTAATGCT 3540
Db 3481 CATCTTTGTTGATACATGAATTAATCAACTGCTGTTTACGAAGGATGATTAATGCT 3540

Oy 3541 CATTTGGGATTTGATTTTCTTCTTATCATACAGGAGAGAGTGA 3586
Db 3541 CATTTGGGATTTGATTTTCTTCTTATCATACAGGAGAGAGTGA 3586

RESULT 3
AF247361 5791 bp DNA linear PRI 26-JUN-2002
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.
DEFINITION AF247361
ACCESSION AF247361.1 GI:19110542
VERSION AF247361.1
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 5791)
Vijh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 5791)
Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
AUTHORS Submitted (21-Mar-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES
source location/Qualifiers
1..5791
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21: between CCR1 and CCR5"
/clone="11a5, frag B"
/cell_type="peripheral blood mononuclear cell"
1..5562
/gene="CCR3"
<249..5562
/gene="CCR3"
/product="CC chemokine receptor 3"
4004..5562
/gene="CCR3"
/product="CC chemokine receptor 3"
4015..5082
/gene="CCR3"
/note="CCR3: G-protein coupled seven transmembrane spanning receptor: principle cell-surface receptor for eotaxin family of chemokines; expressed on eosinophils, CD4/Th2 and CD8 lymphocytes, monocytes, microglia, and dendritic cells"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AA185154.1"
/db_xref="GI:19110543"
/translation="MTSLDVEFEGTSSYYDDVGLCEKADTRALMAQFPPLSLV FTVGLGNVVVMIILIKYRLRIMNLIADLFLVTLPRMIVRGNWVFG HOMCKLISGFYHTGLYSEIFILLTIDRYLAIVHAEFLRATVFGVTSIVMGL AVLAALPEFIEYTELEPEELCSALYEDYVSMRHFRLMTIECLVPLVMAIC YNGILIKTLRPSKRRKYARILIVIMAVEFIEMPRYNVALILSSYSLRENDERS KRLDLMVTEYIAISHCCMNPVITAFVGERKRLRHFFHMLMLGRITPPLPSE KLERSSVSPSTAEPELSTF"

polyA_signal
polyA_site
BASE COUNT 1624 a 1285 c 1160 g 1722 t
ORIGIN

Query Match 97.4%; Score 3494.4; DB 9; Length 5791;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

QY 1 GGAATCCCTACCTTCCCATCAGAGCTAAGGGGCGATGAGCGGCTCTGCTGAAGATGGGA 60
DB 433 GGAATCCCTACCTTCCCATCAGAGCTAAGGGGCGATGAGCGGCTCTGCTGAAGATGGGA 492
QY 61 CCCCCAAGAAATGTCCTCCCTGAGGGGCACTTCCCTACAGATGGATGGAGTGGGTT 120
DB 493 CCCCCAAGAAATGTCCTCCCTGAGGGGCACTTCCCTACAGATGGATGGAGTGGGTT 552
QY 121 AAGTGTGTGTGTCAGCAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCTCGGTTT 180
DB 553 AAGTGTGTGTGTCAGCAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCTCGGTTT 612
QY 181 GTTCATGGCATGGGCGAGGGGTCAAGGAGCAGAGCTTCCCTCAGTCCCTACCAGTGA 240
DB 613 GTTCATGGCATGGGCGAGGGGTCAAGGAGCAGAGCTTCCCTCAGTCCCTACCAGTGA 672
QY 241 GGAAGAGTCATAGCTTGGGCGAGGGGCGAGGGGCGTGGGAGGGGTAGTGGTAACGA 300
DB 673 GGAAGAGTCATAGCTTGGGCGAGGGGCGAGGGGCGTGGGAGGGGTAGTGGTAACGA 732
QY 301 GAGGCGCTCTCCATTCAGCCCAAGAAAGACTAAGATGAATACCTCAGATATATTAGC 360
DB 733 GAGGCGCTCTCCATTCAGCCCAAGAAAGACTAAGATGAATACCTCAGATATATTAGC 792
QY 361 TACAACACACACAGAGAGTTTCCAGAAAAAGGTCAGCGCTTGAGACAGGTCACCCGAC 420
DB 793 TACAACACACACAGAGAGTTTCCAGAAAAAGGTCAGCGCTTGAGACAGGTCACCCGAC 882
QY 421 TCAGCAGACACACAGTATATATAATCAAGACACAAGAGAGACAGAAACACCCCTTCCA 480
DB 853 TCAGCAGACACACAGTATATATAATCAAGAGACACAAGAGAGACAGAAACACCCCTTCCA 912
QY 481 CTCTGCCCATCTGTCTCAAGTGTAGTGGGCTTCTCCAGATCTCTGCCACCTTTAGA 540
DB 913 CTCTGCCCATCTGTCTCAAGTGTAGTGGGCTTCTCCAGATCTCTGCCACCTTTAGA 972
QY 541 AAGGAACACTGAAGAAGAACTGAATATTAAGCTGACAGCATAAAGAGAGTGAATA 600
DB 973 AAGGAACACTGAAGAAGAACTGAATATTAAGCTGACAGCATAAAGAGAGTGAATA 1032
QY 601 ACCTAAATCATTTGTCACATGAATGAATCAGAGAGATTTAAACCACTTTGAGCTAAA 660
DB 1033 ACCTAAATCATTTGTCACATGAATGAATCAGAGAGATTTAAACCACTTTGAGCTAAA 1092
QY 661 TGTGTGAATCTTTTCTCTCTATCCAGCAGATGAGAGAGTGGTAAAGAGACACATA 720
DB 1093 TGTGTGAATCTTTTCTCTCTATCCAGCAGATGAGAGAGTGGTAAAGAGACACATA 1152
QY 721 GTTTGAGAGATAAGAAATCTTGACATTTGCTGAGTTGATTTGATGAATTTTA 780
DB 1153 GTTTGAGAGATAAGAAATCTTGACATTTGCTGAGTTGATTTGATGAATTTTA 1212
QY 781 GTTGACCTCAG-TTTTGTAATCTTGACACAGGGGCAATCCAAATATGCAAGAGATAT 839
DB 1213 GTTGACCTCAGTTTGTGAATCTTGACACAGGG- --CATCATATGTCGAC- AGAGATAT 1268
QY 840 GTTAACCAAGTGAATAGCTGCAATGAGAGAGATTTGGGATTTTACTTGTGTTTTGTC 899
DB 1269 GTTAAC-CAAGTGAATAGCTGCAATGAGAGAGATTTGGGATTTTACTTGTGTTTTGTC 1327
QY 900 TCTTCTTTCTATTTGTTCTTACTTATTTAGATTAACCTATGCTTTCCCAAAATGAAA 959
DB 1328 TCTTCTTTCTATTTGTTCTTACTTATTTAGATTAACCTATGCTTTT-CCAAAATGAAA 1386
QY 960 AGGCAATTTTGAAGCCTAATTCAAACCTTCTCATAATTTTGTATCATAGTATTCACCTT 1019
DB 1387 AGGCAATTTTGAAGCCTAATTCAAACCTTCTCATAATTTTGTATCATAGTATTCACCTT 1446
QY 1020 GATTTGAGACTGGGTAGACAGGTGAAAAACCATATCAGGTTTAAATTTTAAATTTAAT 1079

DB 1447 GATTGAGACTGGGTAGACAGGTGAAAAACCATATCAGGTTTTTAAATTTTAAATTTAAT 1506
QY 1080 TATTATTTATTTATTTATTTTGTGATGAGATCTGGGCTGCGCCAGGCTGAGATGCA 1139
DB 1507 TATTATTTATTTATTTATTTTGTGATGAGATCTGGGCTGCGCCAGGCTGAGATGCA 1566
QY 1140 GCGGCGTGAATCAGATTCACCTGAGGCTCAACCTTTAGGCTCAAGGATTTCTCCACCT 1199
DB 1567 GCGGCGTGAATCAGATTCACCTGAGGCTCAACCTTTAGGCTCAAGGATTTCTCCACCT 1626
QY 1200 CAGCCCCCAAGTAGTTGGACACACAGTATGCGCCACCATGCTTGCTATTTCTTATT 1259
DB 1627 CAGCCCCCAAGTAGTTGGACACACAGTATGCGCCACCATGCTTGCTATTTCTTATT 1686
QY 1260 TTTTGTAGAGATAGGATTCATATATGTCAGGCTGGCTGTAATTCGCGGCTCAG 1319
DB 1687 TTTTGTAGAGATAGGATTCATATATGTCAGGCTGGCTGTAATTCGCGGCTCAG 1746
QY 1320 GTGAGCTCCCACTGGGCTCCCAAGATGATGGAATTAACAGCATAGACCAAGTCCCC 1379
DB 1747 GTGAGCTCCCACTGGGCTCCCAAGATGATGGAATTAACAGCATAGACCAAGTCCCC 1806
QY 1380 TGCCTATGAGATTTTCTGTCTGTATCCCATGACAGTATGATATCAAGACTTGGCTGC 1439
DB 1807 TGCCTATGAGATTTTCTGTCTGTATCCCATGACAGTATGATATCAAGACTTGGCTGC 1866
QY 1440 TGACTGTGAGAGACCTGCAATGCTTCTGTAGCTGTGAACCTGAGTCAAACTCATAG 1499
DB 1867 TGACTGTGAGAGACCTGCAATGCTTCTGTAGCTGTGAACCTGAGTCAAACTCATAG 1926
QY 1500 GCAGCCCTGAACCCCAAAAGGTTCTATGATATCATCTGATCATGTTGATTTT 1559
DB 1927 GCAGCCCTGAACCCCAAAAGGTTCTATGATATCATCTGATCATGTTGATTTT 1986
QY 1560 ATGAATATACACATGAATTAAGACATTAACCTCAAACTGAGCAAAAGCTTAAGTATTT 1619
DB 1987 ATGAATATACACATGAATTAAGACATTAACCTCAAACTGAGCAAAAGCTTAAGTATTT 2046
QY 1620 TTTTAAAGTTTGAACCTGTTTAAATCACCTTGAGAAAAAAGAAATTAATATCAATA 1679
DB 2047 TTTTAAAGTTTGAACCTGTTTAAATCACCTTGAGAAAAAAGAAATTAATATCAATA 2106
QY 1680 ATTAACGGTGAATATACAGGCTATATACCTTTGTTCTCCAGAAATTAACAGTCTGTTCTTT 1739
DB 2107 ATTAACGGTGAATATACAGGCTATATACCTTTGTTCTCCAGAAATTAACAGTCTGTTCTTT 2166
QY 1740 TCTTGTCTTATGATGCTGAATGAGAGAGACACTGTGTATTTGATGTTGATGATA 1799
DB 2167 TCTTGTCTTATGATGCTGAATGAGAGAGACACTGTGTATTTGATGTTGATGATA 2226
QY 1800 AAATGTATATTTTCTTCTAGCTGATGATGATTTGCTATTTATTAAGTAATAAG 1859
DB 2227 AAATGTATATTTTCTTCTAGCTGATGATGATTTGCTATTTATTAAGTAATAAG 2286
QY 1860 CTGATGGAGACACAAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGGCTGG 1919
DB 2287 CTGATGGAGACACAAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGGCTGG 2346
QY 1920 AATGTGCATTTGATCAGTGGGAGATGATCTGAGACAGCCATGAAAGAGATCAACAAG 1979
DB 2347 AATGTGCATTTGATCAGTGGGAGATGATCTGAGACAGCCATGAAAGAGATCAACAAG 2406
QY 1980 TTCCACCAAGGAGACCTATTTTCTTAATTTATTTGAAATGGCTTCTTAATTTGCTCTT 2039
DB 2407 TTCCACCAAGGAGACCTATTTTCTTAATTTATTTGAAATGGCTTCTTAATTTGCTCTT 2466
QY 2040 TTTCATTTCTGCTTCTACAGATTTTACAGCTTTTCTGCTTCAAAATGGAATGCATAT 2099
DB 2467 TTTCATTTCTGCTTCTACAGATTTTACAGCTTTTCTGCTTCAAAATGGAATGCATAT 2526
QY 2100 ACACTCATTTTCTCATACACACCCCAAGTGAACCAATGCTCCTCATTTCGATATA 2159

Db 2527 ACACCTCATTTCCTTCATACCAACCCCAAGTGAACCAATGGCTCCTCATATATA 2586
 Oy 2160 AGTAAGAGAGGCTGTGCATTAAGGCTTGCCAGAGCAGCAGTGAAGGCGGTAGAGAC 2219
 Db 2587 AGTAAGAGAGGCTGTGCATTAAGGCGTGTCCAGAGCAGCAGTGAAGGCGGTAGAGAC 2646
 Oy 2220 TGGCTCATTTCCATCTGTAATTTCTCAGTACCTTGTACCTACCAAGCCCAACATGTGGG 2279
 Db 2647 TGGCTCATTTCCATCTGTAATTTCTCAGTACCTTGTACCTACCAAGCCCAACATGTGGG 2706
 Oy 2280 GCGTCAATTCGATCAATTAATTTCTCAGTACCTTGTACCTACCAAGCCCAACATGTGGG 2339
 Db 2707 GCGTCAATTCGATCAATTAATTTCTCAGTACCTTGTACCTACCAAGCCCAACATGTGGG 2766
 Oy 2340 AGTATTAAGCATTTCTGAGATTTACCTTGAAGAAATGCCATGGCCTGTATATACAT 2399
 Db 2767 AGTATTAAGCATTTCTGAGATTTACCTTGAAGAAATGCCATGGCCTGTATATACAT 2826
 Oy 2400 CTTCACCCCTTGTCCCTCCTCTAGAAAGAGAGAAAGTGAATGCCCTCTGAGAGAC 2459
 Db 2827 CTTCACCCCTTGTCCCTCCTCTAGAAAGAGAGAAAGTGAATGCCCTCTGAGAGAC 2886
 Oy 2460 TAGTCATGCGCTTACCTGCTCTCCATGACTGCTGCTTATCTGTTTCTATTTCTCTCC 2519
 Db 2887 TAGTCATGCGCTTACCTGCTCTCCATGACTGCTGCTTATCTGTTTCTATTTCTCTCC 2946
 Oy 2520 TTTTCACCCGAAGCTATATATCTCAAGAAAGCAGCAGCTGGCCTTAGGGCTCTGGGCT 2579
 Db 2947 TTTTCACCCGAAGCTATATATCTCAAGAAAGCAGCAGCTGGCCTTAGGGCTCTGGGCT 3006
 Oy 2580 AAGAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTGT 2639
 Db 3007 AAGAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTGT 3066
 Oy 2640 CATGAGAGAGCTCCAGAGGCTTGTCTTTTGCATGTATACAGGCTTAACATGACATCAC 2699
 Db 3067 CATGAGAGAGCTCCAGAGGCTTGTCTTTTGCATGTATACAGGCTTAACATGACATCAC 3126
 Oy 2700 AGGGCAGAGAAAGAAAGTAACCTAACTAATGCTGCTTAATTAATTAATTAATTAAT 2759
 Db 3127 AGGGCAGAGAAAGAAAGTAACCTAACTAATGCTGCTTAATTAATTAATTAATTAAT 3186
 Oy 2760 AGTAAATTAATGCTGATGTATGATGTATGAACAGACAAATGTATTTTTCACAGCTGC 2819
 Db 3187 AGTAAATTAATGCTGATGTATGATGTATGAACAGACAAATGTATTTTTCACAGCTGC 3246
 Oy 2820 TGTGATTTGAGTATGATGATTTGGAATTAAGATGCTGTTAAGACACACACAGGCTTC 2879
 Db 3247 TGTGATTTGAGTATGATGATTTGGAATTAAGATGCTGTTAAGACACACACAGGCTTC 3306
 Oy 2880 CTCAAGTCCGTAGCAAAATTTTCAAAAGTAAATTAATTAATTAATTAATTAATTAAT 2939
 Db 3307 CTCAAGTCCGTAGCAAAATTTTCAAAAGTAAATTAATTAATTAATTAATTAATTAAT 3366
 Oy 2940 TGACAGGAGAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2999
 Db 3367 TGACAGGAGAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATG 3426
 Oy 3000 GTTAGAGATTTTGAACAAATTTACTAAATTTCTCAAGTTCAATTTCCCTTAACAT 3059
 Db 3427 GTTAGAGATTTTGAACAAATTTACTAAATTTCTCAAGTTCAATTTCCCTTAACAT 3486
 Oy 3060 AATGAATGCTCATCATATATATGAGGCTCTGAGAGACATTAATTAATTAATTAATTAAT 3119
 Db 3487 AATGAATGCTCATCATATATATGAGGCTCTGAGAGACATTAATTAATTAATTAATTAAT 3546
 Oy 3120 CATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3179
 Db 3547 CATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3606
 Oy 3180 GTAAACTGTAATAAATGCAAAATGCGGTGAAGACAGTAAATTAATTAATTAATTAAT 3239
 Db 3607 GTAAACTGTAATAAATGCAAAATGCGGTGAAGACAGTAAATTAATTAATTAATTAAT 3666

Oy 3240 TTATATTTGTTATCATTTATCTAGCTGTTTCTGTTGTTGTTATTTCTTAAATGC 3299
 Db 3667 TTATATTTGTTATCATTTATCTAGCTGTTTCTGTTGTTGTTATTTCTTAAATGC 3726
 Oy 3300 TTACAGAAATCTGTAATCCCATTTCTACACACACCCACCAACATTTCTGTTCTTTCC 3359
 Db 3727 TTTCAGAAATCTGTAATCCCATTTCTACACACACCCACCAACATTTCTGTTCTTTCC 3786
 Oy 3360 CATGCC -GGTCACTGCTTAATTTGAAGGCTTCACTGCTTTCTCTCAATCTTCTCTG 3418
 Db 3787 CATGCCGGGCTCATGCTTAATTTGAAGGCTTCACTGCTTTCTCTCAATCTTCTCTG 3846
 Oy 3419 GCACCTGATATGCTGCTTTTGAATTTCAATTAAGAAATCCCTAGGCTGCTACATGT 3478
 Db 3847 GCACCTGATATGCTGCTTTTGAATTTCAATTAAGAAATCCCTAGGCTGCTACATGT 3906
 Oy 3479 GGCATCTTTGTTGAGTACATGAATTAATCACTGCTGTTGTTTACGAAGATTAATGC 3538
 Db 3907 GGCATCTTTGTTGAGTACATGAATTAATCACTGCTGTTGTTTACGAAGATTAATGC 3966
 Oy 3539 TTCAATTTGGGATTTGTTATTTTCTTCTTATCAACAGGAGAGATGAA 3586
 Db 3967 TTCAATTTGGGATTTGTTATTTTCTTCTTATCAACAGGAGAGATGAA 4014

RESULT 4
 AC104439
 LOCUS
 DEFINITION Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
 AC104439 AC024739
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 Saenphumachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.,
 and Haugen, E.D.
 Direct Submission
 Unpublished
 2 (bases 1 to 197279)
 Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
 Direct Submission
 Submitted (11-DEC-2001) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 3 (bases 1 to 197279)
 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 Saenphumachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.,
 and Haugen, E.D.
 Direct Submission
 Submitted (20-JUN-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 On Jun 20, 2002 this sequence version replaced gi:17488621.

COMMENT
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 COMMENT

Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: uwgchgs@u.washington.edu
 Drafting Center: WUGSC
 Project Information
 Center project name: chr3
 Center clone name: RP11-793E15 (bc0564)
 Summary Statistics
 Sequencing vector: unknown: 52% of reads
 Sequencing vector: plasmid: 108752: 48% of reads
 Chemistry: Dye-terminator ET: 94% of reads
 Chemistry: Dye-terminator Big Dye: 6% of reads
 Assembly program: Phrap: version 0.990319
 Consensus quality: 197168 bases at least Q40
 Consensus quality: 197255 bases at least Q30

Consensus quality: 197275 bases at least Q20
 Insert size: 197279; sum-of-contigs
 Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-91E8 (UMGC:bc0216) AC026349
 3': CTD-2565A18 (UMGC:bc0730)

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII

BglII

EcoRI

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
-----	-----	-----	-----	-----	-----
2687	2617	8949	8586	8696	8661
-----	-----	-----	-----	-----	-----
6382	6410	2067	2160	6	<800
-----	-----	-----	-----	-----	-----
512	<800	7846	7940	2742	2803
-----	-----	-----	-----	-----	-----
449	<800	3734	3895	5376	5324
-----	-----	-----	-----	-----	-----
2602	2763	1334	1301	1493	1478
-----	-----	-----	-----	-----	-----
2590	2617	2287	2309	823	835
-----	-----	-----	-----	-----	-----
8313	8291	1814	1918	1962	2002
-----	-----	-----	-----	-----	-----
1711	1683	691	<800	2900	2954
-----	-----	-----	-----	-----	-----
9821	9472	5477	5348	1484	1478
-----	-----	-----	-----	-----	-----
516	<800	305	<800	1005	995
-----	-----	-----	-----	-----	-----
8587	8291	25245	25541	1181	1171
-----	-----	-----	-----	-----	-----
7446	7581	3988	4121	18560	19002
-----	-----	-----	-----	-----	-----
2088	2075	1633	1598	3603	3579
-----	-----	-----	-----	-----	-----
2509	2617	631	<800	4943	5076
-----	-----	-----	-----	-----	-----
3519	3501	90	<800	3239	3241
-----	-----	-----	-----	-----	-----

26	<800	402	<800	953	995
-----	-----	-----	-----	-----	-----
925	933	3350	3490	1621	1615
-----	-----	-----	-----	-----	-----
98	<800	4577	4515	6827	6900
-----	-----	-----	-----	-----	-----
6409	6410	1229	1183	79	<800
-----	-----	-----	-----	-----	-----
1383	1376	4221	4331	16418	16263
-----	-----	-----	-----	-----	-----
16048	15829	3980	4121	3361	3241
-----	-----	-----	-----	-----	-----
1876	1877	2548	2497	872	881
-----	-----	-----	-----	-----	-----
4169	4068	674	<800	4220	4193
-----	-----	-----	-----	-----	-----
1674	1683	2332	2309	2848	2803
-----	-----	-----	-----	-----	-----
52	<800	11445	11045	2283	2318
-----	-----	-----	-----	-----	-----
5227	5082	5692	5632	3211	3241
-----	-----	-----	-----	-----	-----
15464	15829	1385	1414	4615	4632
-----	-----	-----	-----	-----	-----
14333	14296	608	<800	6823	6900
-----	-----	-----	-----	-----	-----
1026	1026	3930	3895	886	881
-----	-----	-----	-----	-----	-----
645	<800	1465	1414	2032	2002
-----	-----	-----	-----	-----	-----
6621	6410	2382	2497	8680	8661
-----	-----	-----	-----	-----	-----
8413	8291	747	<800	5163	5076
-----	-----	-----	-----	-----	-----
1401	1376	1951	2012	1547	1478
-----	-----	-----	-----	-----	-----
1512	1471	642	<800	7058	6900
-----	-----	-----	-----	-----	-----
5801	5644	21060	21003	1647	1615
-----	-----	-----	-----	-----	-----
3256	3278	3700	3666	2753	2803
-----	-----	-----	-----	-----	-----
3448	3501	1321	1301	162	<800
-----	-----	-----	-----	-----	-----
2738	2763	10705	10502	1078	1093
-----	-----	-----	-----	-----	-----
237	<800	3128	3317	2156	2173
-----	-----	-----	-----	-----	-----
6715	6823	183	<800	5077	5076
-----	-----	-----	-----	-----	-----
201	<800	3255	3490	154	<800
-----	-----	-----	-----	-----	-----
1002	1026	5693	5632	1571	1478
-----	-----	-----	-----	-----	-----
221	<800	3380	3317	219	<800
-----	-----	-----	-----	-----	-----
2854	2899	237	<800	520	<800
-----	-----	-----	-----	-----	-----
6998	7317	431	<800	1540	1478
-----	-----	-----	-----	-----	-----
1174	1145	2152	2160	1479	1478
-----	-----	-----	-----	-----	-----
7876	8291	249	<800	1613	1615
-----	-----	-----	-----	-----	-----
1911	1877	2599	2778	1399	1478
-----	-----	-----	-----	-----	-----
3899	3847	685	<800	9553	9383
-----	-----	-----	-----	-----	-----
5672	5644	41	<800	166	<800
-----	-----	-----	-----	-----	-----
1711	1683	388	<800	13615	13115
-----	-----	-----	-----	-----	-----
862	854	2500	2497	4731	4632

	-----	2368	2389	2889	2778	5159	5076
	-----	-----	-----	178	<800	4503	4430
	-----	-----	-----	6589	6728	6607	6900
	-----	-----	-----	3836	3895	2766	2803
Query Match 97.4%; Score 3492.8; DB 9; Length 197279;							
Best Local Similarity 99.4%; Pred. No. 0;							
Matches 3568; Conservative 0; Mismatches 12; Indels 8; Gaps 6;							
QY	1	GGATCCCTACCTTCCCATACAGCTAGAGGGGCGATGAGCGCTCTCTGTAGATGGGA	60				
DB	186606	GGATCCCTACCTTCCCATACAGCTAGAGGGGCGATGAGCGCTCTCTGTAGATGGGA	186665				
QY	61	CCCCAAGGAATGTCTCCCTGTGGGGCACTTCTTACAGATGGATGGCCAGTGGTT	120				
DB	186666	CCCCAAGGAATGTCTCCCTGTGGGGCACTTCTTACAGATGGATGGCCAGTGGAGTT	186725				
QY	121	AAGTTGTGTGTAGGCGAGAAAAAAGATCTAGTTTGTACTTGTAGAGTTTCCGGTTT	180				
DB	186726	AAGTTGTGTGTAGGCGAGAAAAAAGATCTAGTTTGTACTTGTAGAGTTTCCGGTTT	186785				
QY	181	GTTCAATGCGATGGGAGGAGCTCAAGAGACAGCACCCTTGCCTCAGTGCCTACAGTGA	240				
DB	186786	GTTCAATGCGATGGGAGGAGCTCAAGAGACAGCACCCTTGCCTCAGTGCCTACAGTGA	186845				
QY	241	GGAAAAAGTGATAGCTTGGGCGCAGGGCCCTGGTGAGGCGTATGTTGTAACAGA	300				
DB	186846	GGAAAAAGTGATAGCTTGGGCGCAGGGCCCTGGTGAGGCGTATGTTGTAACAGA	186905				
QY	301	GAGGCTCTCCATTTCCAGCCCAAGAGACATAAGATTAATCTTCATGATATATTAC	360				
DB	186906	GAGGCTCTCCATTTCCAGCCCAAGAGACATAAGATTAATCTTCATGATATATTAC	186965				
QY	361	TACAAACCCACGACAGGTTCCAGAAAAAGGCTGAGGTTGAAGCCAGTACCCCCAC	420				
DB	186966	TACAAACCCACGACAGGTTCCAGAAAAAGGCTGAGGTTGAAGCCAGTACCCCCAC	187025				
QY	421	TCAGAGACACCAAGTCTATATAATCAAGAGACCAAGAGACAGAACCCCTTCCCA	480				
DB	187026	TCAGAGACACCAAGTCTATATAATCAAGAGACCAAGAGACAGAACCCCTTCCCA	187085				
QY	481	CTCTGCCCATGTCTCAAGTTTACTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA	540				
DB	187086	CTCTGCCCATGTCTCAAGTTTACTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA	187145				
QY	541	AAGGAACACTGAAGAAGAACTGAATTTATAGCTGACAGATTAAGAGGATGATGA	600				
DB	187146	AAGGAACACTGAAGAAGAACTGAATTTATAGCTGACAGATTAAGAGGATGATGA	187205				
QY	601	ACCTAAATCATTTGTTCAATGAATGAATCAAGAGAAGTTTAAACACTTTGGACTAAA	660				
DB	187206	ACCTAAATCATTTGTTCAATGAATGAATCAAGAGAAGTTTAAACACTTTGGACTAAA	187265				
QY	661	TGTGTGAATCTTTTCTTCTGCTATCCAGACAGATGAAGAGCTGTAAACAGACCAATA	720				
DB	187266	TGTGTGAATCTTTTCTTCTGCTATCCAGACAGATGAAGAGCTGTAAACAGACCAATA	187325				
QY	721	GTTTGAGACTGAAGAATCATTTGACATTTTCACTGCTGATGTGATGATTAATTTTA	780				
DB	187326	GTTTGAGACTGAAGAATCATTTGACATTTTCACTGCTGATGTGATGATTAATTTTA	187385				
QY	781	GTTGACCTTAC-TTTGTAATCTTGCACACGGGCAATCTATATCTGCACAAGATAT	839				
DB	187386	GTTGACCTTAC-TTTGTAATCTTGCACACGGG---CATCCATATCTGCAC-AGAGATAT	187441				
QY	840	GTTAAACAGTGTAAATGCTGCATGAGAGATTGGGTGATTTTAACTTTTGTTTGTGC	899				
DB	187442	GTTAA-CAGTGTAAATGCTGCATGAGAGATTGGGTGATTTTAACTTTTGTTTGTGC	187500				

QY	900	TCTTCTTCTATTTGTCTTACTTATTTACGATTAACCCATGCTTTTCCCAAAATGTAAA	959				
DB	187501	TCTTCTTCTTATTTGTCTTACTTATTTACGATTAACCCATGCTTTT-CCAAAAAGTAAA	187559				
QY	960	AGGCATTTTGAAGCCTAATTCAAACCTTCTCAGTATTTTGTATCTAAGTATCACCTT	1019				
DB	187560	AGGCATTTTGAAGCCTAATTCAAACCTTCTCAGTATTTTGTATCTAAGTATCACCTT	187619				
QY	1020	GATTGAGACTGGGTAGACAGGTGAAGAACCAATTCAGGTTTTTAAATTTTAAAT	1079				
DB	187620	GATTGAGACTGGGTAGACAGGTGAAGAACCAATTCAGGTTTTTAAATTTTAAAT	187679				
QY	1080	TATTTATTTATTTATTTTATTTTGAATGAGTGTGGCTGCGCCAGCGGTGAGTGA	1139				
DB	187680	TATTTATTTATTTATTTTATTTTGAATGAGTGTGGCTGCGCCAGCGGTGAGTGA	187739				
QY	1140	GCGGCGTGTACACAGTTCACTGACCTTCACCTTCATGAGGCTCAAGGATTTCTCCACT	1199				
DB	187740	GCGGCGTGTATCACAGTTCACTGACCTTCACCTTCATGAGGCTCAAGGATTTCTCCACT	187799				
QY	1200	CAGCCCCCAAGTATGTGGGACACACGATATGCCACCATGCTTGGCTAATTTCTTAT	1259				
DB	187800	CAGCCCCCAAGTATGTGGGACACACGATATGCCACCATGCTTGGCTAATTTCTTAT	187859				
QY	1260	TTTTTGTAGAGTATAGATCTCATATTGTTCAGGCTGCTGTAAATTTCTGGGCTCAG	1319				
DB	187860	TTTTTGTAGAGTATAGATCTCATATTGTTCAGGCTGCTGTAAATTTCTGGGCTCAG	187919				
QY	1320	GTAGACCTCCCACTGGGCTCCCAAGAGTACGGATTAACAGCATAGAGCCAAAGTCCCC	1379				
DB	187920	GTAGACCTCCCACTGGGCTCCCAAGAGTACGGATTAACAGCATAGAGCCAAAGTCCCC	187979				
QY	1380	TGCCATATGAGATTTTCTCTCTGATCCATGCACTAGTAAATCAAGACTTGGCTGC	1439				
DB	187980	TGCCATATGAGATTTTCTCTCTGATCCATGCACTAGTAAATCAAGACTTGGCTGC	188039				
QY	1440	TGACGTGGAGAGCTGCATGCTTCTTGAGGCTGAGACTTCAAGTCAAAAGCTCATAG	1499				
DB	188040	TGACGTGGAGAGCTGCATGCTTCTTGAGGCTGAGACTTCAAGTCAAAAGCTCATAG	188099				
QY	1500	GCAGCCCTGAAGCCCAAAACCAAAAGTTCTATGAGTTTATCATCTGATCATGTGATTTT	1559				
DB	188100	GCAGCCCTGAAGCCCAAAACCAAAAGTTCTATGAGTTTATCATCTGATCATGTGATTTT	188159				
QY	1560	ATAGAATTAACATGATTAATTAAGACACTACCTCAAACTGAGCAAAACTTAAGTAATT	1619				
DB	188160	ATAGAATTAACATGATTAATTAAGACACTACCTCAAACTGAGCAAAACTTAAGTAATT	188219				
QY	1620	TTTTTAAAGTTTGAACCTGTTTTTAAATCACTCTTGGAGAAAAAGAAAAATTAATACAAATA	1679				
DB	188220	TTTTTAAAGTTTGAACCTGTTTTTAAATCACTCTTGGAGAAAAAGAAAAATTAATACAAATA	188279				
QY	1680	ATTAACGGTAATPACAGGCTACTATACCTTGTCTCCGAATTPAGCAGTTCTGTTCTTT	1739				
DB	188280	ATTAACGGTAATPACAGGCTACTATACCTTGTCTCCGAATTPAGCAGTTCTGTTCTTT	188339				
QY	1740	TCTTCTTTAGATGCTGAAGTGCAGAGAGACACTGTGTGATTTGACGTGTACTGACA	1799				
DB	188340	TCTTCTTTAGATGCTGAAGTGCAGAGAGACACTGTGTGATTTGACGTGTACTGACA	188399				
QY	1800	AAATGTATTTTTTTTTTCTCACCTGCTATGATGATGATTAATGATTAATTAAGTAAGT	1859				
DB	188400	AAATGTATTTTTTTTTTCTCACCTGCTATGATGATGATTAATGATTAATTAAGTAAGT	188459				
QY	1860	CTGATGGAGACACACAACCATTTGTTCTCAGTCTCATCTTTCTCCCTCAAAACCTGG	1919				
DB	188460	CTGATGGAGACACACAACCATTTGTTCTCAGTCTCATCTTTCTCCCTCAAAACCTGG	188519				
QY	1920	AATGTGCCATTGATAGTGGAGATGTACCTTGACAGACCCATGAAAAAGATCAACAAG	1979				
DB	188520	AATGTGCCATTGATAGTGGAGATGTACCTTGACAGACCCATGAAAAAGATCAACAAG	188579				

QY 1980 TTCACCCAGAGGACCCCTATTTTCTATTTGTAATGCTTCTATTTGCTTC 2039
| | | | |
Db 188580 TTCACCCAGAGGACCCCTATTTTCTATTTGTAATGCTTCTATTTGCTTC 188639
QY 2040 TTTCATTTCTGCTCTCTACAGATTTTACAGCTTTTCTGTTTCAATGGAATGCAT 2099
| | | | |
Db 188640 TTTCATTTCTGCTCTCTACAGATTTTACAGCTTTTCTGTTTCAATGGAATGCAT 188699
QY 2100 ACACCTTCATTTTCTCTACACAAACCCCAAGTGAACCAATGGTCTCTCATTTGCATATA 2159
| | | | |
Db 188700 ACACCTTCATTTTCTCTACACAAACCCCAAGTGAACCAATGGTCTCTCATTTGCATATA 188759
QY 2160 AGTAAGAGGAGCTCTGATTAAGGCTTTGCCAGGACGAGCTGAGAGGGCTTAGAC 2219
| | | | |
Db 188760 AGTAAGAGGAGCTCTGATTAAGGCTTTGCCAGGACGAGCTGAGAGGGCTTAGAC 188819
QY 2220 TGGCTCATTTTCATCTATCTCTACGCTTGTGACTTACCAGAACCCCAACATGTGGG 2279
| | | | |
Db 188820 TGGCTCATTTTCATCTATCTCTACGCTTGTGACTTACCAGAACCCCAACATGTGGG 188879
QY 2280 GCTCAGATTTGATCAATTTATTTAAGAGCAAAACAAATTTCCCGCATTTGGCCC 2339
| | | | |
Db 188880 GCTCAGATTTGATCAATTTATTTAAGAGCAAAACAAATTTCCCGCATTTGGCCC 188939
QY 2340 AGTTATTAAAGCATTTCTCAGATTTACCTTGAGAAATGCCATGGCTGTATTTACAT 2399
| | | | |
Db 188940 AGTTATTAAAGCATTTCTCAGATTTACCTTGAGAAATGCCATGGCTGTATTTACAT 188999
QY 2400 CTTCACCTTTGCTCCCTCCCTCAGAAAGAGAAAGTCAAGTTGGATGGCTCGTAGAAG 2459
| | | | |
Db 189000 CTTCACCTTTGCTCCCTCCCTCAGAAAGAGAAAGTCAAGTTGGATGGCTCGTAGAAG 189059
QY 2460 TAGTGATGAGCTTAACGTCTTCATGATGATGCTGCTTATCTGTTTCTATTTTCTCC 2519
| | | | |
Db 189060 TAGTGATGAGCTTAACGTCTTCATGATGATGCTGCTTATCTGTTTCTATTTTCTCC 189119
QY 2520 TTTTCCACCGAAGTCTATATCTCAGAAAGAGAGCATGGCTTAGGGCTCTGGCT 2579
| | | | |
Db 189120 TTTTCCACCGAAGTCTATATCTCAGAAAGAGAGCATGGCTTAGGGCTCTGGCT 189179
QY 2580 AAGAAATATCAAGTCCAGAGAGAAATCCCATTTGACTGACCCCTCGCTTATCCCTTGT 2639
| | | | |
Db 189180 AAGAAATATCAAGTCCAGAGAGAAATCCCATTTGACTGACCCCTCGCTTATCCCTTGT 189239
QY 2640 GATGAGAAAGCTCCAGAGGCTTTGCTTTTGCATTTTACAGAGCTTACTGACATCAC 2699
| | | | |
Db 189240 GATGAGAAAGCTCCAGAGGCTTTGCTTTTGCATTTTACAGAGCTTACTGACATCAC 189299
QY 2700 AGGGGCAAGAAAGAAAGTAACTAACTAATGCTGCTTATATTTGTAATTTGTAAT 2759
| | | | |
Db 189300 AGGGGCAAGAAAGAAAGTAACTAACTAATGCTGCTTATATTTGTAATTTGTAAT 189359
QY 2760 AGTTAATTTACTGATTTGATGATGTAACAGCAAAATGTGTAATTTTTCACAGCTGC 2819
| | | | |
Db 189360 AGTTAATTTACTGATTTGATGATGTAACAGCAAAATGTGTAATTTTTCACAGCTGC 189419
QY 2820 TGTGATTTGATTTTATGCAATTTGGAATTAAGATGCTTTAAGACACACAGCCAGGTT 2879
| | | | |
Db 189420 TGTGATTTGATTTTATGCAATTTGGAATTAAGATGCTTTAAGACACACAGCCAGGTT 189479
QY 2880 CTCGAATCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATACATCTGAACTCTGAG 2939
| | | | |
Db 189480 CTCGAATCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATACATCTGAACTCTGAG 189539
QY 2940 TCACAGAGAAATGACATGATAGAGACTAAAGATCTAGCCCAATTTTATTTACTT 2999
| | | | |
Db 189540 TCACAGAGAGAAATGACATGATAGAGACTAAAGATCTAGCCCAATTTTATTTACTT 189599
QY 3000 GTTAGAGGATTTTGAACAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAACAT 3059
| | | | |
Db 189600 GTTAGAGGATTTTGAACAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAACAT 189659
QY 3060 AATGAATGTCTCATCTTTATGGGGCCCTGGAGAGCATTAATTTACTTGTATTTGTAATAT 3119

Db 189660 AATGAATGTCTCATCTTTATGGGGCCCTGGAGAGCATTAATTTACTTGTATTTGTAATAT 189719
| | | | |
QY 3120 CATTTGTTATTTATTTATATATTTTATTTTGTCTTTTAAATGATTAAGGATATAT 3179
| | | | |
Db 189720 CATTTGTTATTTATTTATATTTTATTTTGTCTTTTAAATGATTAAGGATATAT 189779
| | | | |
QY 3180 GTAAACTGTAAACATTAATAATGCAAAATGCGTAGAGACAGTAAATTAATGATTA 3239
| | | | |
Db 189780 GTAAACTGTAAACATTAATAATGCAAAATGCGTAGAGACAGTAAATTAATGATTA 189839
| | | | |
QY 3240 TTATATTTGTTATCATTTATCTAGCTGTTTTTTCCTGTTGTGATTTTCTTTAAATGC 3299
| | | | |
Db 189840 TTATATTTGTTATCATTTATCTAGCTGTTTTTTCCTGTTGTGATTTTCTTTAAATGC 189899
| | | | |
QY 3300 TTAACAAATCTGTATCCCATTTTTCACACACACCCCAACATTTTGTGCTTTTCC 3359
| | | | |
Db 189900 TTTCAAAATCTGTATCCCATTTTTCACACACACCCCAACATTTTGTGCTTTTCC 189959
| | | | |
QY 3360 CATGCC-GGTCAATGCTAATTTGAAAGCTTCAGCTCTTCCATCAATCTCTCCG 3418
| | | | |
Db 189960 CATGCCGGGTCAATGCTAATTTGAAAGCTTCAGCTCTTCCATCAATCTCTCCG 190019
| | | | |
QY 3419 GCACCTGTATATGCTTTTGAATTCATGTTAAGATTCCTAGGCTGCTATCATGT 3478
| | | | |
Db 190020 GCACCTGTATATGCTTTTGAATTCATGTTAAGATTCCTAGGCTGCTATCATGT 190079
| | | | |
QY 3479 GGCATCTTTGTTGAGTACATGATTAATCACTGGTGTGTTTACGAAGATGATTAATGC 3538
| | | | |
Db 190080 GGCATCTTTGTTGAGTACATGATTAATCACTGGTGTGTTTACGAAGATGATTAATGC 190139
| | | | |
QY 3539 TTTCATTTGGGATTTGATTTTCTTCTTCTATTCACAGGAGAGTGA 3586
| | | | |
Db 190140 TTTCATTTGGGATTTGATTTTCTTCTTCTATTCACAGGAGAGTGA 190187
| | | | |
RESULT 5
HSA312688 220965 bp DNA linear HTG 15-MAY-2002
LOCUS HSA312688
DEFINITION Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, ***
ACCESSION AJ312688.2 GI:13559235
VERSION AJ312688.2
KEYWORDS HTG; HTGS_PHASE2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Kiss,H., Yang,Y., Kiss,C., Andersson,K., Klein,G., Imreh,S. and
Dumanski,J.P.
The transcriptional map of the common eliminated region 1 (C3CER1)
in 3p21.3
Eur J Hum. Genet. 10 (1), 52-61 (2002)
MEDLINE 21906202
PUBMED 11896456
TITLE 2 (bases 1 to 220965)
REFERENCE Kiss,H.
AUTHORS Direct Submission
TITLE Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology
JOURNAL Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
COMMENT
On Apr 5, 2001 this sequence version replaced gi:13548633.
The sequence is a consensus sequence of clone RP4-787c23 (1-140400
bp).
clone RP6-32g23 (31212-220965 bp), clone RP6-146el (partially,
1-6800 bp)
and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
contigs are
in order and the gaps between them are represented by 100 Ns.
Contig 1:
1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
Contig 4:

28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
Contig 7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:
11756-118727 bp
Contig 10: 118628-121834 bp Contig 11: 121935-127855 bp Contig
12:
127956-129383 bp Contig 13: 129484-131747 bp Contig 14:
131848-132316 bp
Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig
17:
135628-189051 bp Contig 18: 189152-189476 bp Contig 19:
189577-191375 bp
Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig
22:
202408-204878 bp Contig 23: 204979-213531 bp Contig 24:
213632-218109 bp
Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 11731: contig of 11731 bp in length
11732 11831: gap of 100 bp
11832 26218: contig of 14387 bp in length
26219 26318: gap of 100 bp
26319 28347: contig of 2029 bp in length
28348 28447: gap of 100 bp
28448 42160: contig of 13713 bp in length
42161 42360: gap of 200 bp
42361 55059: contig of 12699 bp in length
55060 55159: gap of 100 bp
55160 61578: contig of 6419 bp in length
61579 61678: gap of 100 bp
61679 97342: contig of 35664 bp in length
97343 97442: gap of 100 bp
97443 117655: contig of 20213 bp in length
117656 117755: gap of 100 bp
117756 118727: contig of 972 bp in length
118728 118827: gap of 100 bp
118828 121834: contig of 3007 bp in length
121835 121934: gap of 100 bp
121935 127855: contig of 5921 bp in length
127856 127955: gap of 100 bp
127956 129383: contig of 1428 bp in length
129384 129483: gap of 100 bp
129484 131747: contig of 2264 bp in length
131748 131847: gap of 100 bp
131848 132316: contig of 469 bp in length
132317 132416: gap of 100 bp
132417 134455: contig of 2039 bp in length
134456 134555: gap of 100 bp
134556 135527: contig of 972 bp in length
135528 135627: gap of 100 bp
135628 189051: contig of 53424 bp in length
189052 189151: gap of 100 bp
189152 189476: contig of 325 bp in length
189477 189576: gap of 100 bp
189577 191375: contig of 1799 bp in length
191376 191475: gap of 100 bp
191476 201473: contig of 9998 bp in length
201474 201573: gap of 100 bp
201574 202307: contig of 734 bp in length
202308 202407: gap of 100 bp
202408 204878: contig of 2471 bp in length
204879 204978: gap of 100 bp
204979 213531: contig of 8553 bp in length
213532 213631: gap of 100 bp
213632 218109: contig of 4478 bp in length

FEATURES
source
1. 220965
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21.3"
/clone="RP6-32g23"
BASE COUNT 62577 a 44674 c 45661 g 65453 t 2600 others
ORIGIN
Query Match 97.1% Score 3481.6; DB 2; Length 220965;
Best Local Similarity 99.4% Pred. No. 0;
Matches 3568; Conservative 0; Mismatches 9; Indels 11; Gaps 7;
QY 1 GGAATCCCTACCTTCCCATGAGAGCTAAGGGGATGGAGCGCTCTCTGTAAGATGGGGA 60
|||||
Db 136685 GGAATCCCTACCTTCCCATGAGAGCTAAGGGGATGGAGCGCTCTCTGTAAGATGGGGA 136744
QY 61 CCCCCAAGAAATGTCCTCGTGGGCGACTTCCTTACAGATGGATGGCCAGTCGGTT 120
|||||
Db 136745 CCCCCAAGAAATGTCCTCGTGGGCGACTTCCTTACAGATGGATGGCCAGTCAGTT 136804
QY 121 AAGTTGGTGTGACGAGCAAAAAAAGATCTAGTTGTACTGTGAGAGTTCTCGGTTT 180
|||||
Db 136805 AAGTTGGTGTGACGAGCAAAAAAAGATCTAGTTGTACTGTGAGAGTTCTCGGTTT 136864
QY 181 GTTCATGCGATGGGCGAGGAGTCAGAGCAGAGCTTCTCTAGTGCCTACAGTGCA 240
|||||
Db 136865 GTTCATGCGATGGGCGAGGAGTCAGAGCAGAGCTTCTCTAGTGCCTACAGTGCA 136924
QY 241 GGAAGAGTCATAGCTGGGCCAGGGCCAGGGCCCTGTGTGAGCGCTAGTGTAACAGA 300
|||||
Db 136925 GGAAGAGTCATAGCTGGGCC---GCCAGGGCCCTGTGTGAGCGCTAGTGTAACAGA 136981
QY 301 GAGGGCTCTCATTCACGCCCAAGGAAGATAAGAAATACCTCATGAGTATATTAGC 360
|||||
Db 136982 GAGGGCTCTCATTCACGCCCAAGGAAGATAAGAAATACCTCATGAGTATATTAGC 137041
QY 361 TACAAACACACAGCAGGTTCCAGAAAAAGCTCAGCTTGGACAGGTCACCCCCAC 420
|||||
Db 137042 TACAAACACACAGCAGGTTCCAGAAAAAGCTCAGCTTGGACAGGTCACCCCCAC 137101
QY 421 TCAGCAGACACGCTATATAATCAAGACCAACAGAGACAGGAACCCCTTCCCA 480
|||||
Db 137102 TCAGCAGACACGCTATATAATCAAGACCAACAGAGACAGGAACCCCTTCCCA 137161
QY 481 CTCTGCCCATGTCATAGTTGTAAGTGGCCCTCTCCACATCTCAGCCACATCTTAGA 540
|||||
Db 137162 CTCTGCCCATGTCATAGTTGTAAGTGGCCCTCTCCACATCTCAGCCACATCTTAGA 137221
QY 541 AAGGAACACTGAAAGAAACTGAATTAATTAAGCTGACAGCTTAAAGAGATGAGTAAA 600
|||||
Db 137222 AAGGAACACTGAAAGAAACTGAATTAATTAAGCTGACAGCTTAAAGAGATGAGTAAA 137281
QY 601 ACCTAAATCATTTGTCATGATGAATCAAGAGAAGATTAAACCACTTTGACTTAAAA 660
|||||
Db 137282 ACCTAAATCATTTGTCATGATGAATCAAGAGAAGATTAAACCACTTTGACTTAAAA 137341
QY 661 TGTGTGAATCCTTTTCCCTGCTATCCAGCAGATGAGAAAGCTGTATACAGAGCAATAA 720
|||||
Db 137342 TGTGTGAATCCTTTTCCCTGCTATCCAGCAGATGAGAAAGCTGTATACAGAGCAATAA 137401
QY 721 GTTTGAGACTAAAGAAATCTTGCATTTGACATGCTGAGTGTATATGAGTAATTTTA 780
|||||
Db 137402 GTTTGAGACTAAAGAAATCTTGCATTTGACATGCTGAGTGTATATGAGTAATTTTA 137461
QY 781 GTTGACCTCAC-TTTGTAATCTTGCAACAGGGGCAATTCATATCTGCAACAAGATAT 839
|||||
Db 137462 GTTGACCTCAC-TTTGTAATCTTGCAACAGGGG---CATCATATCTGCAAC-AGAGATAT 137517

QY	840	GTAAACAGTGTGTAATCTCTGCATGAGAGATTTGGGATTTTTTACTTTCGTTTTGTGC	899
Db	137518	GTAAA-CAGTGGTAATCTCTGCATGAGAGATTTGGGATTTTTTACTTTCGTTTTGTGC	137576
QY	900	TCTTCTTCTTAATGTCGTCTACTATTAGCATTAACCTTCGTGTTTTCCAAATGTAA	959
Db	137577	TCTTCTTCTTAATGTCGTCTACTATTAGCATTAACCTTCGTGTTTTCCAAATGTAA	137635
QY	960	AGGCCATTTTGAAGCCTAATTCAAACCTCTCTACATATTTTGATCTAAGTATTCACCTT	1019
Db	137636	AGGCCATTTTGAAGCCTAATTCAAACCTCTCTACATATTTTGATCTAAGTATTCACCTT	137695
QY	1020	GATTGAGACTGGGTGAGACAGGTGAAGAAACCATATAGGTATTTTAAATTTTAAAT	1079
Db	137696	GATTGAGACTGGGTGAGACAGGTGAAGAAACCATATAGGTATTTTAAATTTTAAAT	137755
QY	1080	TATTTTATTTTATTTATTTATTTTGTAGATGAGCTGGCTGTGCCAGGCTGAGATGCA	1139
Db	137756	TATTTTATTTTATTTATTTATTTTGTAGATGAGCTGGCTGTGCCAGGCTGAGATGCA	137815
QY	1140	GGGGGTATACAGTTCACGTACGTGACGCCCTAACCTTCTTAGGCTCAAGGATTTCCACCT	1199
Db	137816	GGGGGTATACAGTTCACGTACGTGACGCCCTAACCTTCTTAGGCTCAAGGATTTCCACCT	137875
QY	1200	CAGCCCCCAAGTAGTTCGGGACACAGTATGCGCCACCATAGGCTGGCTAATTTCTAAT	1259
Db	137876	CAGCCCCCAAGTAGTTCGGGACACAGTATGCGCCACCATAGGCTGGCTAATTTCTAAT	137935
QY	1260	TTTTTGTAGAGATAGGATCTCACTATATTTGTCCAGGCTGCTTTGAATTCGTGGCTCAG	1319
Db	137936	TTTTTGTAGAGATAGGATCTCACTATATTTGTCCAGGCTGCTTTGAATTCGTGGCTCAG	137995
QY	1320	GTGAGCCTTCCACACGTGGGCTCTCCCAAAGTACTGGGATTTACAGGATAGCCAGAGTCCCC	1379
Db	137996	GTGAGCCTTCCACACGTGGGCTCTCCCAAAGTACTGGGATTTACAGGATAGCCAGAGTCCCC	138055
QY	1380	TGCCCATATGAGATTTTCTGTCTCTGATCCCATGACAGTATCAAGGACTTGGCTGC	1439
Db	138056	TGCCCATATGAGATTTTCTGTCTCTGATCCCATGACAGTATCAAGGACTTGGCTGC	138115
QY	1440	TGACCTGTGAGAGACTGATGCTTTCTTGAGCTGTGAACCTCAAGTGTAAACCTCATAG	1499
Db	138116	TGACCTGTGAGAGACTGATGCTTTCTTGAGCTGTGAACCTCAAGTGTAAACCTCATAG	138175
QY	1500	GCAGCCCTGAACCCCAACCAAAAGTTCATGTTTTATCATCTCTGATCATGTTGATTTT	1559
Db	138176	GCAGCCCTGAACCCCAACCAAAAGTTCATGTTTTATCATCTCTGATCATGTTGATTTT	138235
QY	1560	ATGAGAAATPACACATGATTTAAACACCTAACCCCAACACGAGCAAACTTAAGTAATTT	1619
Db	138236	ATGAGAAATPACACATGATTTAAACACCTAACCCCAACACGAGCAAACTTAAGTAATTT	138295
QY	1620	TTTTTAACTTTGACCTGTTTTTAAATACACTCTTGAGAAAAAGGAAATTAATACAAATA	1679
Db	138296	TTTTTAACTTTGACCTGTTTTTAAATACACTCTTGAGAAAAAGGAAATTAATACAAATA	138355
QY	1680	ATTAAACGCTGAATPACAGCTCTATPACCTTTGTTCTCCAGAAATTTAGCAGTTCTGTTCTTT	1739
Db	138356	ATTAAACGCTGAATPACAGCTCTATPACCTTTGTTCTCCAGAAATTTAGCAGTTCTGTTCTTT	138415
QY	1740	TCTTCTTTAGTGTGTAAGTGCAAGGAGACATCTGATTTAGTGTGTAAGTGCA	1799
Db	138416	TCTTCTTTAGTGTGTAAGTGCAAGGAGACATCTGATTTAGTGTGTAAGTGCA	138475
QY	1800	AAATGTGATTTTTTTTCTCAGCTGCTATGGATGGATTTAGTATTAATTAATGAATG	1859
Db	138476	AAATGTGATTTTTTTTCTCAGCTGCTATGGATGGATTTAGTATTAATTAATGAATG	138535
QY	1860	CTGATGGGAGACACACAAACCATTTGTTGCTCAGTCCATTTTCTCTTAAGAGCCTGG	1919
Db	138536	CTGATGGGAGACACACAAACCATTTGTTGCTCAGTCCATTTTCTCTTAAGAGCCTGG	138595

QY	1920	AATGTGCCATTGTATCAGTGGGAGATGTATACCTCGACACAGCCATGTAAAGATTCACACAG	13979
Db	138596	AATGTGCCATTGTATCAGTGGGAGATGTATACCTCGACACAGCCATGTAAAGATTCACACAG	1386555
QY	1980	TTCCACCCCAAGGAGCCCATTTTTCCTAAATTTCATTTGAAATGGCTCTAATTGTCCCTTC	2039
Db	138656	TTCCACCCCAAGGAGCCCATTTTTCCTAAATTTCATTTGAAATGGCTCTAATTGTCCCTTC	138715
QY	2040	TTTCAATTCCCTGCTTCCTAACAGGTTTTTACAGCTTTTTCTGGTTTCAATGTGAACCTCACAT	2099
Db	138716	TTTCAATTCCCTGCTTCCTAACAGGTTTTTACAGCTTTTTCTGGTTTCAATGTGAACCTCACAT	138775
QY	2100	ACACATCATTTTTCCTCATCACACCCCAAGTCACCCAAATGTGCTCCATCTTTCGATATA	2159
Db	138776	ACACATCATTTTTCCTCATCACACCCCAAGTCACCCAAATGTGCTCCATCTTTCGATATA	138835
QY	2160	AGTAAAGAGGCTCTGCATTAAGGGCTTTTCCAAAGGACCGACGCTGAGAGGGCTTAGGAC	2219
Db	138836	AGTAAAGAGGCTCTGCATTAAGGGCTTTTCCAAAGGACCGACGCTGAGAGGGCTTAGGAC	1388955
QY	2220	TGGCTCCATTTTCATCTCATCTTATTCACAGTCTTTCAGTACCTTACCCAGAACCCCAATGTGGG	2279
Db	138896	TGGCTCCATTTTCATCTCATCTTATTCACAGTCTTTCAGTACCTTACCCAGAACCCCAATGTGGG	1389555
QY	2280	GCCCTCAGATTCGATCAATTAATTTATTAAGAACCAAAACAATTTCCCCCATTTGGCCCC	2339
Db	138956	GCCCTCAGATTCGATCAATTAATTTATTAAGAACCAAAACAATTTCCCCCATTTGGCCCC	139015
QY	2340	AGTTATTAAGCATTTCTCAGATTTTACCTTGTAGAAATGCCATGGGCTGTATATTCACAT	2399
Db	139016	AGTTATTAAGCATTTCTCAGATTTTACCTTGTAGAAATGCCATGGGCTGTATATTCACAT	139075
QY	2400	CTTCAACCTTGTCCCTCTCTCTGAAAGAGAAAGTCAGTTGGATCCCTCGAGAGAAC	2459
Db	139076	CTTCAACCTTGTCCCTCTCTCTCTGAAAGAGAAAGTCAGTTGGATCCCTCGAGAGAAC	139135
QY	2460	TATGTCACTGCTTAACTGTCTCTCCATCATGACTCTGGCCTATCTGTGTTTCTAATTTCCCTCC	2519
Db	139136	TATGTCACTGCTTAACTGTCTCTCCATCATGACTCTGGCCTATCTGTGTTTCTAATTTCCCTCC	139195
QY	2520	TTTTCCACCGAAGTCATTAATCTCAAGAAAGACAGGACAGGGCCTTATGGGCTCTGGCCT	2579
Db	139196	TTTTCCACCGAAGTCATTAATCTCAAGAAAGACAGGACAGGGCCTTATGGGCTCTGGCCT	139255
QY	2580	AAGAAATATCAAGTCACAGTGAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTTGT	2639
Db	139256	AAGAAATATCAAGTCACAGTGAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTTGT	139315
QY	2640	GATGAGAGAGCTCCACGAGGGTTTCTTTTGCATGTACCAAGGCTTACACACATCAC	2699
Db	139316	GATGAGAGAGCTCCACGAGGGTTTCTTTTGCATGTACCAAGGCTTACACACACATCAC	139375
QY	2700	AGGGCAGAGAAAGAAAGTAACTAACTAATCTGCTCTTATATTTGTAATTTATTTGTAAT	2759
Db	139376	AGGGCAGAGAAAGAAAGTAACTAACTAATCTGCTCTTATATTTGTAATTTATTTGTAAT	139435
QY	2760	AGTTATTAATCTGTGATTTTACATGTGTACAGACACAAATGTGTAATTTTTCACAGCTGC	2819
Db	139436	AGTTATTAATCTGTGATTTTACATGTGTACAGACACAAATGTGTAATTTTTCACAGCTGC	139495
QY	2820	TGTGATTTGGATTTATGACCATTTTGGAAATTAAGAAATCTGTGTAAGAGCACACAAGCCAGTTTC	2879
Db	139496	TGTGATTTGGATTTATGACCATTTTGGAAATTAAGAAATCTGTGTAAGAGCACACAAGCCAGTTTC	139555
QY	2880	CTCAAGTCCGTAAGCAAAATTTTTCAAAAGTTAAATTTAAAAATCATACATTTGAAATCTAG	2939
Db	139556	CTCAAGTCCGTAAGCAAAATTTTTCAAAAGTTAAATTTAAAAATCATACATTTGAAATCTAG	139615
QY	2940	TGACAGGAGAAATGGACATGTGATAGACACTAAGATCTTACCCCAATTTTATATTACTT	2999
Db	139616	TGACAGGAGAAATGGACATGTGATAGACACTAAGATCTTACCCCAATTTTATATTACTT	139675
QY	3000	GTTAAGCATTTTTCGAACAATTTACTAAATTTTCTTCAAGGTTTCAATTTCCCATTAATCTAT	3059

```
|||||
Db 139676 GTTAGAGATTTTGACAAATTAATTAATTTCTCAAGGTTCAATTTCCCATTAATCTAT 139735
QY 3060 AATGAATGCTCATCTATTTAGGGCCCTGGAGAGCATATTAATCTGTAATTAAT 3119
Db 139736 AATGAATGCTCATCTATTTAGGGCCCTGGAGAGCATATTAATCTGTAATTAAT 139795
QY 3120 CATTTGTAATTAATTAATTAATTTGCTTTTAATGATTAATTTTAAGTATAT 3179
Db 139796 CATTTGTAATTAATTAATTAATTTGCTTTTAATGATTAATTTTAAGTATAT 139855
QY 3180 GTAAGCTGTAAGCAATTAATGCAAAATGCCGTAGAGACAGTAAATTAATTAATGA 3239
Db 139856 GTAAGCTGTAAGCAATTAATGCAAAATGCCGTAGAGACAGTAAATTAATGA 139915
QY 3240 TTATATTTGTAATTAATTAATTAATTTGCTTTTAATGATTAATTTTAAGTATAT 3299
Db 139916 TTATATTTGTAATTAATTAATTAATTTGCTTTTAATGATTAATTTTAAGTATAT 139975
QY 3300 TTACAGAAATCTGTATCCCATCTTCCACACACCCACAAATTTGCTTTTCCTTTCC 3359
Db 139976 TTTCAGAAATCTGTATCCCATCTTCCACACACCCACAAATTTGCTTTTCCTTTCC 140035
QY 3360 CATGCC-GGTCATGCTAATCTTTGAAAGCTTCAGCTCTTCTCTCAATCTTCTCCTG 3418
Db 140036 CATGCCGGGTCATGCTAATCTTTGAAAGCTTCAGCTCTTCTCTCAATCTTCTCCTG 140095
QY 3419 GCACCTCTGATATGCTTTTGAATCATGTTAAAGATCCCTAGCTGCTATCAATGT 3478
Db 140096 GCACCTCTGATATGCTTTTGAATCATGTTAAAGATCCCTAGCTGCTATCAATGT 140155
QY 3479 GGCATCTTTGTTGAGTACATGAATTAATCACTGCTGTGTTTACGAGAGATGATTATGC 3538
Db 140156 GGCATCTTTGTTGAGTACATGAATTAATCACTGCTGTGTTTACGAGAGATGATTATGC 140215
QY 3539 TTCATTTGTTGAGATTTGATTTTCTTCTCTATCACAGGAGAAATGAA 3586
Db 140216 TTCATTTGTTGAGATTTGATTTTCTTCTCTATCACAGGAGAAATGAA 140263

RESULT 6
AF224496S2 7010 bp DNA linear PRI 02-MAY-2001
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 2 and
DEFINITION partial cds.
ACCESSION AF224497.1 GI:13924486
VERSION AF224497.1
KEYWORDS 2 of 2
SEGMENT Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7010)
AUTHORS Scotell,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 7010)
AUTHORS Scotell,E.J.
TITLE Direct Submision
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
FEATURES
source
1.7010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/order(AF224496.1:298..957,1..>7010)
/gene="CCR3"
/join(AF224496.1:298..376,6784..>7010)
/gene="CCR3"
/product="CC chemokine receptor 3"
repeat_region 4318..4570
```

```
/rpl_family="Alu"
/rpl_type=dispersed
6784..7010
/gene="CCR3"
number=2
6795..>7010
/gene="CCR3"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AAK49028.1"
/db_xref="GI:13924487"
/translation="MTSLDITVEFTGTTSYVDVGLCEKADTRALMQFVPLSLV
FVGLGNVVMILIKYRRLRMNIY"
BASE COUNT 2136 a 1420 c 1320 g 2129 t 5 others
ORIGIN
Query Match 95.1%; Score 3408.6; DB 9; Length 7010;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3563; Conservative 1; Mismatches 16; Indels 16; Gaps 13;
QY 1 GATCCCTACCTTCCCATCAGAGCTTAGGGGGCATGGAGGCTCTGCTAAGATGGGA 60
Db 3205 GGATCCCTACCTTCCCATCAGAGCTTAGGGGGCATGGAGGCTCTGCTAAGATGGGA 3264
QY 61 CCCCAAGAAATGTCCTCCCTGTGGGCACCTTACACAGATGGAGTGGCGGTT 120
Db 3265 CCCCAAGAAATGTCCTCCCTGTGGGCACCTTACACAGATGGAGTGGCGGTT 3324
QY 121 AAGTTGGTGCAGGCGAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCTCGGTTT 180
Db 3325 AAGTTGGTGCAGGCGAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCTCGGTTT 3384
QY 181 GTTCATGAGCATGGGCGAGGGAGTCAAGAGACAGACCTTCCCTCATGCTTACCAGTGCA 240
Db 3385 GTTCATGAGCATGGGCGAGGGAGTCAAGAGACAGACCTTCCCTCATGCTTACCAGTGCA 3444
QY 241 GGAAGAGTGCATAGCTTGAGGCCAGGCGCCAGGSCCTGTGGAGAGCTAGTGGTAACAGA 300
Db 3445 GGAAGAGTGCATAGCTTGAGGCCAGGCGCCAGGSCCTGTGGAGAGCTAGTGGTAACAGA 3504
QY 301 GAGGGCTCTCCATTCAGCCCAAGAAAGATTAAGATGAATACCTCATGATATATTAGC 360
Db 3505 GAGGGCTCTCCATTCAGCCCAAGAAAGATTAAGATGAATACCTCATGATATATTAGC 3564
QY 361 TACAAACACACACAGCAGAGTTCAGAAAAAGGCTCAGCTTGGACACAGTCAACCCAC 420
Db 3565 TACAAACACACACAGCAGAGTTCAGAAAAAGGCTCAGCTTGGACACAGTCAACCCAC 3624
QY 421 TCAGACAGACACAGTCATATTAATCAAGACACAAAGAGAGACAGAAACACCCCTTCCCA 480
Db 3625 TCAGACAGACACAGTCATATTAATCAAGACACAAAGAGAGACAGAAACACCCCTTCCCA 3684
QY 481 CTCTGCCCATGTCCTCAAGTTGTAAGTGGCCCTTCTCCAGATCTTGCCACATCTTAGA 540
Db 3685 CTCTGCCCATGTCCTCAAGTTGTAAGTGGCCCTTCTCCAGATCTTGCCACATCTTAGA 3744
QY 541 AAGGAACACTGAAAGAAAGAACTGAATTTAAGCTGACAGCATTAAGAGAGATGAGTAAA 600
Db 3745 AAGGAACACTGAAAGAAAGAACTGAATTTAAGCTGACAGCATTAAGAGAGATGAGTAAA 3804
QY 601 ACCTAAATCATTTGTCATCATGATGAATCAAGAGAACTTAACACCTTTGGACTAAA 660
Db 3805 ACCTAAATCATTTGTCATCATGATGAATCAAGAGAACTTAACACCTTTGGACTAAA 3864
QY 661 TGTGTGAATCTTTTCTGCTATCCAGCAGATGAGAAAGCTGTAAACAGACACACATA 720
Db 3865 TGTGTGAATCTTTTCTGCTATCCAGCAGATGAGAAAGCTGTAAACAGACACACATA 3924
QY 721 GTTTGGAGACTAAAGATCTTTGACATTTCACTG-CTGAGTGTATTTGAGATTAATTTT 779
Db 3925 GTTTGGAGACTAAAGATCTTTGACATTTCACTGCTGAGTGTATTTGAGATTAATTTT 3984
QY 780 AGTTGACCTCAC-TTTGTAATCTTGACACAGGGGCAATCAATATCTGCACAAGAGATA 838
```

```
||||| 3985 AGTTGACCTCATTCTGTAGATCTTGCACAGGG---CATCCATATCTGCAC-AGAGATA 4040
||||| 839 TGTTAACCAAGGTAATGCGATGAGAGATGGGTGATTTTACTTTCGTTTGTG 898
||||| 4041 TGTAA--CAGGGTAATGCGCATGAGAGATGGGTGATTTTACTTTCGTTTGTG 4099
CTCTCTCTCTCTATTTGTTCTTACTTATTTAGATTACCTATCGTTTCCAAATGTAA 958
4100 CTCTCTCTCTCTATTTGTTCTTACTTATTTAGATTACCTATCGTTT-CCAAATGTAA 4158
QY 959 AAGGCCATTTGAAAGCCTTAATCAACCTCTTCACATTTTGTATCTAAGTATTCACCT 1018
||||| 4159 AAGGCCATTTGAAAGCCTTAATCAACCTCTTCACATTTTGTATCTAAGTATTCACCT 4218
QY 1019 TGAATTGAGCTGGGTAGACAGGTGAACCATATCAGTCTTTTAAATTTTAA 1078
||||| 4219 TGATTGAGCTGGGTAGACAGGTGAACCATATCAGGCTTTTAAATTTTAA 4278
QY 1079 TTAATTTATTTATTTATTTTATTTTGTAGATGAGTCTGGCTGTCGCCAGGCTGAGTGC 1138
||||| 4279 TTAATTTATTTATTTATTTATTTTGTAGATGAGTCTGGCTGTCGCCAGGCTGAGTGC 4338
QY 1139 AGGGCGTGTATCAGAGTTCACGTGAGCCTCAACCTTCTAGGCTCAAGGATTCCTCAC 1198
||||| 4339 AGGGCGTGTATCAGAGTTCACGTGAGCCTCAACCTTCTAGGCTCAAGGATTCCTCAC 4398
QY 1199 TCAGCCCCCAAGTAGTTGGAGCACACGTATGGCCACCATTGGCTGATTTCTTAT 1258
||||| 4399 TCAGCCCCCAAGTAGTTGGAGCACACGTATGGCCACCATTGGCTGATTTCTTAT 4458
QY 1259 TTTTGTGTAGAGATAGATCTCATTATTTGTCAGAGCTGGTCTGTAATTCCTGGGCTCA 1318
||||| 4459 TTTTGTGTAGAGATAGATCTCATTATTTGTCAGAGCTGGTCTGTAATTCCTGGGCTCA 4518
QY 1319 GGTGAGCCTCCACCTGGGCTCCCAAGTACTGGGATTTACAGGCAATGAG--CCAAGTCC 1377
||||| 4519 GGTGAGCCTCCACCTGGGCTCCCAAGTACTGGGATTTACAGGCAATGAGCCCAAGTCC 4578
QY 1378 CCGGCCATATGAGATTTTCTGCTGATCCCATG--CAGTAGTATTCAGAGCATTTGGC 1436
||||| 4579 CCGGCCATATGAGATTTTCTGCTGATCCCATGAGCAGTATTAACAAGGCTTGGC 4638
QY 1437 TCGTACTGTGAGAGACCTCATGCTTCTGTAGCTGTGAACCTCAGTGTAAAGCTCA 1496
||||| 4639 TCGTACTGTGAGAGACCTCATGCTTCTGTAGCTGTGAACCTCAGTGTAAAGCTCG 4698
QY 1497 TAGGCACCCCTGAACCCCAAAAGGTTCTATGTTTATCTCTGATCATGTTGAT 1556
||||| 4699 TAGGCACCCCTGAACCCCAAAAGGTTCTATGTTTATCTCTGATCATGTTGAT 4758
QY 1557 TTTATAGAAATTAACACATGATTTAAAGACACTACCTCAAACTGAGCAAAACCTTAAGTAA 1616
||||| 4759 TTTATAGAAATTAACACATGATTTAAAGACACTACCTCAAACTGAGCAAAACCTTAAGTAA 4818
QY 1617 TTTTGTAAAGTTGACCTGTTTTTAAATCACTCTTGAGAAAAAGAAAAATAATACAA 1676
||||| 4819 TTTTGTAAAGTTGACCTGTTTTTAAATCACTCTTGAGAAAAAGAAAAATAATACAA 4878
QY 1677 ATATATTAGGGTGAATCAGGCTACTATACCTTTGTTCTCCAGAAATAGAGTTCTGTTG 1736
||||| 4879 ATATATTAGGGTGAATCAGGCTACTATACCTTTGTTCTCCAGAAATAGAGTTCTGTTG 4938
QY 1737 TTTTCTCTCTTATGATCTGAAGTGCAGAAAGACACTCTGATTTGACGTTGTAACCTG 1796
||||| 4939 TTTTCTCTCTTATGATCTGAAGTGCAGAAAGACACTCTGATTTGACGTTGTAACCTG 4998
QY 1797 ACAAAATGTATTTTCTCTCAGCTGCTATGATTTGATTTGATTTATGATTTAGATA 1856
||||| 4999 ACAAAATGTATTTTCTCTCAGCTGCTATGATTTGATTTGATTTATGATTTAGATA 5058
QY 1857 ATGCTGATGGAGACACACAAACCATTTGTTCTCAGTCCATTTTCTCTCAAAAGCC 1916
|||||

5059 ATGCTGATGGAGACACACAAACCATTTGTTCTCAGTCCATTTTCTCTCAAAAGCC 5118
QY 1917 TGGAAATGTCATTGATGACATGGGAGATGATACCTGGACACAGCATTAAGAGATCAAC 1976
||||| 5119 TGGAAATGTCATTGATGACATGGGAGATGATACCTGGACACAGCATTAAGAGATCAAC 5178
QY 1977 AAGTTCACCCCAAGGAGACCTTAATTTTCCAAATTTCTTAAATGATGCTTCT--AATGTGTC 2035
||||| 5179 AAGTTCACCCCAAGGAGACCTTAATTTTCCAAATTTCTTAAATGATGCTTCTAATTTGTC 5238
QY 2036 CTTCCTTCAATTCCTGCTTCTTACACAGTTTATACACTTTTCTGCTTCT--AAATGTGACT 2094
||||| 5239 CTTCCTTCAATTCCTGCTTCTTACACAGTTTATACACTTTTCTGCTTCTGCTTCTAATTTGACT 5298
QY 2095 CACATACACTCTCATTTTCTCTCATCAACCCCAAGTCCCAATGCTCCACTTCTG 2154
||||| 5299 CACATACACTCTCATTTTCTCTCATCAACCCCAAGTCCCAATGCTCCACTTCTG 5358
QY 2155 ATATTAAGTAAAGAGGCTGTGATTAAGGCTTGTCCAAAGGACAGAGTGAAGG--CG 2212
||||| 5359 ATATTAAGTAAAGAGGCTGTGATTAAGGCTTGTCCAAAGGACAGAGTGAAGGCTG 5418
QY 2213 CTAGAGATGCTCTCATTTCCATCTCTATTTCTACTGACTTTGACTACCCGAAACCCCAAC 2272
||||| 5419 CTAGAGATGCTCTCATTTCCATCTCTATTTCTCACTGACTTTGACTACCCGAAACCCCAAC 5478
QY 2273 ATGAGGGGCTCAGTATTTGATGATCAATTAATTTAAGGCAAAACATTTCCCGCAT 2332
||||| 5479 ATGAGGGGCTCAGTATTTGATGATCAATTAATTTAAGGCAAAACATTTCCCGCAT 5538
QY 2333 TGGCCCCAGTTATTAAGCATTTTCTCAGATTTTACCTTGAGAAATGCCATGGGCTGTATA 2392
||||| 5539 TGGCCCCAGTTATTAAGCATTTTCTCAGATTTTACCTTGAGAAATGCCATGGGCTGTATA 5598
QY 2393 TTCACTCTTCAACCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2452
||||| 5599 TTCACTCTTCAACCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5658
QY 2453 GAGGAATAGAGCATGAGCTTAACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2512
||||| 5659 GAGGAATAGAGCATGAGCTTAACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5718
QY 2513 TTCTCTCTTTTCCACCGAAGCTTAATTAATCTCAAGAAAAAGCAGCAGTGGCTTAGGGCTC 2572
||||| 5719 TTCTCTCTTTTCCACCGAAGCTTAATTAATCTCAAGAAAAAGCAGCAGTGGCTTAGGGCTC 5778
QY 2573 CTGGCCCTAAGAAATATCAAGTCCAGTGAAGATCCCTTACGTACCCCTGCTTAC 2632
||||| 5779 CTGGCCCTAAGAAATATCAAGTCCAGTGAAGATCCCTTACGTACCCCTGCTTAC 5838
QY 2633 CCTTTGTGATGAGAAAGCTCCCAAGGGGTTGCTTTTGTGATTTACAGGCTCAACCTCAG 2692
||||| 5839 CCTTTGTGATGAGAAAGCTCCCAAGGGGTTGCTTTTGTGATTTACAGGCTCAACCTCAG 5898
QY 2693 CATTCACGAGGGGCAAGAAAGAAAGTAACTTAACCTTAACCTTAATGCTTATTAATTTGAATTA 2752
||||| 5899 CATTCACGAGGGGCAAGAAAGAAAGTAACTTAACCTTAACCTTAATGCTTATTAATTTGAATTA 5958
QY 2753 TTGTAAATAGTTAATTTACTGATTTGTATGATGTGAACAGCAAAAGTGTATTTTTC 2812
||||| 5959 TTGTAAATAGTTAATTTACTGATTTGTATGATGTGAACAGCAAAAGTGTATTTTTC 6018
QY 2813 CAGCTGCTGTGATGATGATTTATGCAATTTGGAATTAAGAAAGCTTAAGAGCAACAGC 2872
||||| 6019 CAGCTGCTGTGATGATGATTTATGCAATTTGGAATTAAGAAAGCTTAAGAGCAACAGC 6078
QY 2873 CAGGTTCTCAAGTCCGTACCAATTTTTCAAAAGTTTAAATTTAAATCTACATCAATTTG 2932
||||| 6079 CAGGTTCTCAAGTCCGTACCAATTTTTCAAAAGTTTAAATTTAAATCTACATCAATTTG 6138
QY 2933 AATCTAGTACAGAGAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2992
||||| 6139 AATCTAGTACAGAGAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6198
|||||
```

QY 2993 TTTACTGTAGAGATTTTGAACAATTACTAAATTTCTTCAGGTTCAATTTCCCAT 3052
|||||
Db 6199 TTTACTGTAGAGATTTTGAACAATTACTAAATTTCTTCAGGTTCAATTTCCCAT 6258
QY 3053 TTAACATATGAATGATCTCATCATTTATGAGGCGCTGGAGACATTAATTTACTGTAAATG 3112
|||||
Db 6259 TTAACATATGAATGATCTCATCATTTATGAGGCGCTGGAGACATTAATTTACTGTAAATG 6318
QY 3113 TTAATATCATTTGTATTTATTTATATACATTTTCTTTTAAATGATTAAGATTTTAA 3172
|||||
Db 6319 TTAATATCATTTGTATTTATTTATATATACATTTTCTTTTAAATGATTAAGATTTTAA 6378
QY 3173 GGTATATGAACCTGTAACAAATGCAAAATGCCCTAAGACAGACTAGTAATTAATA 3232
|||||
Db 6379 GGTATATGAACCTGTAACAAATGCAAAATGCCCTAAGACAGACTAGTAATTAATA 6438
QY 3233 ATGATTTATTAATTTGTATTCATATCTAGCCGTTTTCTGTGTATTTCTTCTCT 3292
|||||
Db 6439 ATGATTTATTAATTTGTATTCATATCTAGCCGTTTTCTGTGTATTTCTTCTCT 6498
QY 3293 TTAATGCTTACGAATCTGATTTCCCATTC-TTCACCAACACCCCAACATTTCTGCT 3351
|||||
Db 6499 TTAATGCTTACGAATCTGATTTCCCATTCATCCACCAACCAATTTCTGCT 6558
QY 3352 TCTTTTCCCATGCC-GGTCATGCTAACTTTGAAGCTTCAGCTTTCTTCTCAATCC 3410
|||||
Db 6559 TCTTTTCCCATGCCGGGTCATCTTAACCTTTGAAGCTTCAGCTTTCTTCTCAATCC 6618
QY 3411 TTTCTCCCTGGACCTCTGATATGCTTTTGAATTCATGTTAAGAATCCCTAGGCTGCTA 3470
|||||
Db 6619 TTTCTCCCTGGACCTCTGATATGCTTTTGAATTCATGTTAAGAATCCCTAGGCTGCTA 6678
QY 3471 TCACATGTCGATCTTTGTGATGATCAATTAATCAACCTGCTGTTTTCGAAGGAT 3530
|||||
Db 6679 TCACATGTCGATCTTTGTGATGATCAATTAATCAACCTGCTGTTTTCGAAGGAT 6738
QY 3531 GATTATGCTTCATTTGGGATTTGATTTTCTTCTTCTATCACAGGAGAGATGAA 3586
|||||
Db 6739 GATTATGCTTCATTTGGGATTTGATTTTCTTCTTCTATCACAGGAGAGATGAA 6794

RESULT 7
AF237380S2 3388 bp DNA linear PRI 05-OCT-2000

LOCUS AF237380S2 Homo sapiens CCR3 gene and exon 3.
DEFINITION AF237381
ACCESSION AF237381.1 GI:10643653
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 3388)
Zimmermann,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y.,
Moulton,E.A. and Rothenberg,M.E.
Analysis of the CC chemokine receptor 3 gene reveals a complex 5'
exon organization, a functional role for untranslated exon 1, and a
broadly active promoter with eosinophil-selective elements
Blood 96 (7), 2346-2354 (2000)

JOURNAL
MEDLINE
PUBMED
20458773
11001881
REFERENCE
AUTHORS
2 (bases 1 to 3388)
Daugherty,B.L.
TITLE
Direct Submission
Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research
Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA
JOURNAL
TITLE
Location/Qualifiers
1..3388
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"

/map="3p21"
/clone="427-G2"
/clone.lib="BamHI + HindIII fragment from phage P1 genomic
library (DMPC-HFF No. 1; Genome Systems, Inc., St. Louis,
MO)"
order(AF237380.1:1..2895,1..3388)
/gene="CCR3"
/note="CC chemokine receptor 3"
join(AF237380.1:1552..1642,2816..>2884)
/gene="CCR3"
mRNA
1104..1384
/note="Alu-J subfamily consensus"
/rpl_family="Alu"
/rpl_type="dispersed
2816..2884
/gene="CCR3"
exon
BASE COUNT 956 a 744 c 663 g 1025 t
ORIGIN
Query Match 94.5%; Score 3388; DB 9; Length 3388;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCCCTACCTTCCCATCAGAGCTAGGGGCGATGAGCGCTCTCTCTAGATGGGA 60
|||||
Db 1 GGATCCCTACCTTCCCATCAGAGCTAGGGGCGATGAGCGCTCTCTCTAGATGGGA 60
QY 61 CCCCCAAGAAATGTCCTCCCTGTGGGGCACTTCTTACAGATGGATGGCCAGTGGCTT 120
|||||
Db 61 CCCCCAAGAAATGTCCTCCCTGTGGGGCACTTCTTACAGATGGATGGCCAGTGGCTT 120
QY 121 AAGTTGGTGTGACGAGCAAAAAAAGATCTAGTTGTCTCTGTGAGATTCTCGGTTT 180
|||||
Db 121 AAGTTGGTGTGACGAGCAAAAAAAGATCTAGTTGTCTCTGTGAGATTCTCGGTTT 180
QY 181 GTTCATGGCATGGGCGAGGAGTCAAGAGACAGACAGCTTGCCTCAGTGCATCAATGCA 240
|||||
Db 181 GTTCATGGCATGGGCGAGGAGTCAAGAGACAGACAGCTTGCCTCAGTGCATCAATGCA 240
QY 241 GGAAGAAAGTGCAATAGCTTGGGCCAGGGCCCTGTGTGAGGCTGTAGTGAACAGA 300
|||||
Db 241 GGAAGAAAGTGCAATAGCTTGGGCCAGGGCCCTGTGTGAGGCTGTAGTGAACAGA 300
QY 241 GGAAGAAAGTGCAATAGCTTGGGCCAGGGCCCTGTGTGAGGCTGTAGTGAACAGA 300
|||||
Db 241 GGAAGAAAGTGCAATAGCTTGGGCCAGGGCCCTGTGTGAGGCTGTAGTGAACAGA 300
QY 301 GAGGGCTCTCCATTCACAGCCCAAGGAAGACTAAGATGAATACCTCATAGTATATTAGC 360
|||||
Db 301 GAGGGCTCTCCATTCACAGCCCAAGGAAGACTAAGATGAATACCTCATAGTATATTAGC 360
QY 361 TACAACACACACAGAGAGGTTCCAGAAAAAGGCTCAGCTTGGAAACAGTCAACCCAC 420
|||||
Db 361 TACAACACACACAGAGAGGTTCCAGAAAAAGGCTCAGCTTGGAAACAGTCAACCCAC 420
QY 421 TCAGCAGACACAGATCATTAATCAAGAGACCAAGAGACAGAGAACACCCCTTCCCA 480
|||||
Db 421 TCAGCAGACACAGATCATTAATCAAGAGACCAAGAGAGACAGAGAACACCCCTTCCCA 480
QY 481 CTTGCGCCCATGTCCTCAATGTTAGTGCGCTTCCCTCCAGATCTCTGCCACCATCTTACA 540
|||||
Db 481 CTTGCGCCCATGTCCTCAATGTTAGTGCGCTTCCCTCCAGATCTCTGCCACCATCTTACA 540
QY 541 AAGGAACACTGAAGAAGAACTGAATTAAGTGCAGCAGCATAAAGAGATGAATAA 600
|||||
Db 541 AAGGAACACTGAAGAAGAACTGAATTAAGTGCAGCAGCATAAAGAGATGAATAA 600
QY 601 ACCCTAAATCATTTGTTACATGATGAATCAAGAGAGTTTAACCATCTTGGACTAATA 660
|||||
Db 601 ACCCTAAATCATTTGTTACATGATGAATCAAGAGAGTTTAACCATCTTGGACTAATA 660
QY 661 TGTGTAATCTTTTCTTCTGCTATCCAGCAGATGAGAACTGTATACAGAGACACATAA 720
|||||
Db 661 TGTGTAATCTTTTCTTCTGCTATCCAGCAGATGAGAACTGTATACAGAGACACATAA 720
QY 721 GTTGGAGACTAAGAAATCATTCACATTTCACTGCTGAGTTGTATTTGAGTAAATTTTA 780

|||||
Db 721 GTTTGAGAGCTAAAGATCATTCACATTTCACTGCTGAGTTGATGAGTAATTTTA 780
OY 781 GTTGACCTACCTTTGTAATCTTGACAGGGGCGCATTCATATCTGACCAAGATATG 840
Db 781 GTTGACCTACCTTTGTAATCTTGACAGGGGCGCATTCATATCTGACCAAGATATG 840
OY 841 TTAAACAGTGTAAATGCTGCATGAGAGATTTGGTATTTTACTTCTGTTTTGTGCT 900
Db 841 TTAAACAGTGTAAATGCTGCATGAGAGATTTGGTATTTTACTTCTGTTTTGTGCT 900
OY 901 CTTCCTTTCTATTTGTTCTTACTTATTTAGATTTACCTATCGTTTCCCAAAATGTA 960
Db 901 CTTCCTTTCTATTTGTTCTTACTTATTTAGATTTACCTATCGTTTCCCAAAATGTA 960
OY 961 GGGCATTGTAAGAGCTTAATTCAAACCTCTTCACTATTTTGATATCAAGTATTCACCT 1020
Db 961 GGGCATTGTAAGAGCTTAATTCAAACCTCTTCACTATTTTGATATCAAGTATTCACCT 1020
OY 1021 ATTGAGACTGGGTAGACAGGTGAAACCATATTCAGGTTTTTAATTTTAAATTTTAA 1080
Db 1021 ATTGAGACTGGGTAGACAGGTGAAACCATATTCAGGTTTTTAATTTTAAATTTTAA 1080
OY 1081 ATTTATTTATTTATTTATTTTGGATGAGATGCTGGCTGCGCCAGGCTGAGTGAC 1140
Db 1081 ATTTATTTATTTATTTATTTTGGATGAGATGCTGGCTGCGCCAGGCTGAGTGAC 1140
OY 1141 CGGCGTATGATCAGATTCAGTCACTGAGCCGCAACCTTTAGGCTCAAGGATTCGCGCAC 1200
Db 1141 CGGCGTATGATCAGATTCAGTCACTGAGCCGCAACCTTTAGGCTCAAGGATTCGCGCAC 1200
OY 1201 AGGCCCCCAAGTATTTGGGACACACAGTATGCGCACCATGCTGGCTAATTTCTTAT 1260
Db 1201 AGGCCCCCAAGTATTTGGGACACACAGTATGCGCACCATGCTGGCTAATTTCTTAT 1260
OY 1261 TTTTGTAGATGAGATTCACATATATTTCCAGGCTGCTGTTGAATTTCTGGGCTCAG 1320
Db 1261 TTTTGTAGATGAGATTCACATATATTTCCAGGCTGCTGTTGAATTTCTGGGCTCAG 1320
OY 1321 TGAGCCTCCACCTGGGCGCTCCCAAGTATCTGGATTTACAGGATGAGCCAAAGTCC 1380
Db 1321 TGAGCCTCCACCTGGGCGCTCCCAAGTATCTGGATTTACAGGATGAGCCAAAGTCC 1380
OY 1381 GCCCATATGAGATTTCTGCTGTGATCCCATGACGTAATTCAGAGACTTGCTGCT 1440
Db 1381 GCCCATATGAGATTTCTGCTGTGATCCCATGACGTAATTCAGAGACTTGCTGCT 1440
OY 1441 GACTCTGGAGAGCTGCATGCTTTCTGAGCTGTAACCTTCAATGCTCAATAGG 1500
Db 1441 GACTCTGGAGAGCTGCATGCTTTCTGAGCTGTAACCTTCAATGCTCAATAGG 1500
OY 1501 CAGCCCTGAAACCCAAACCAAAAGTTCTATGTTTATCTATCCGTGATGATGATTT 1560
Db 1501 CAGCCCTGAAACCCAAACCAAAAGTTCTATGTTTATCTATCCGTGATGATGATTT 1560
OY 1561 TAGAAATTAACATGATTAAGACACTTACCTCAAACTGAGCAAACTTAAGTAATTT 1620
Db 1561 TAGAAATTAACATGATTAAGACACTTACCTCAAACTGAGCAAACTTAAGTAATTT 1620
OY 1621 TTTTAAGTTGACCTGTTTTTAATCACTTTTGAGAGAAAAGAAAATAATCAATA 1680
Db 1621 TTTTAAGTTGACCTGTTTTTAATCACTTTTGAGAGAAAAGAAAATAATCAATA 1680
OY 1681 TTAAAGGTGACCTGTTTTTAATCACTTTTGAGAGAAAAGAAAATAATCAATA 1740
Db 1681 TTAAAGGTGACCTGTTTTTAATCACTTTTGAGAGAAAAGAAAATAATCAATA 1740
OY 1741 CTTCGTTTATGATGCTGTAAGTGCAGAAAGACACTCTGTGATTTGATGCTGTAAGTGC 1800
Db 1741 CTTCGTTTATGATGCTGTAAGTGCAGAAAGACACTCTGTGATTTGATGCTGTAAGTGC 1800
OY 1801 AATGTGATTTTCTGAGCTGCTATGATTTGATTTATGATTAAGAAATGC 1860
Db 1801 AATGTGATTTTCTGAGCTGCTATGATTTGATTTATGATTAAGAAATGC 1860

Db 1801 AATGTGATTTTCTGAGCTGCTATGATTTGATTTATGATTAAGAAATGC 1860
OY 1861 TGATGGAGACACACAAACCATTTGTTCTCATGCTCATTTTCTCTCAAAAGCTGGA 1920
Db 1861 TGATGGAGACACACAAACCATTTGTTCTCATGCTCATTTTCTCTCAAAAGCTGGA 1920
OY 1921 ATGTGCATTGATCACTGGGAGATGACCTGAGACAGACCCATGMAAAGATCAACAGT 1980
Db 1921 ATGTGCATTGATCACTGGGAGATGACCTGAGACAGACCCATGMAAAGATCAACAGT 1980
OY 1981 TCCACCAAGGAGCCCTATTTTCTCAATTTTCAATTTGAAATGGCTCTATATGCTCT 2040
Db 1981 TCCACCAAGGAGCCCTATTTTCTCAATTTTCAATTTGAAATGGCTCTATATGCTCT 2040
OY 2041 TTCAATTCGCTCTCCATCCAGTTTTCACGTTTTCGTTTCAATTTGAAATGAACTCA 2100
Db 2041 TTCAATTCGCTCTCCATCCAGTTTTCACGTTTTCGTTTCAATTTGAAATGAACTCA 2100
OY 2101 CACTCTCATTTTCTCATACACACCCCAAGTACCCCAATGCTCTCACTTTGATATTA 2160
Db 2101 CACTCTCATTTTCTCATACACACCCCAAGTACCCCAATGCTCTCACTTTGATATTA 2160
OY 2161 GTTAAGGAGCTCTGCATTAAGGCTTTGTCGAAGCAGCAGCTGAGAGGCTTAGACT 2220
Db 2161 GTTAAGGAGCTCTGCATTAAGGCTTTGTCGAAGCAGCAGCTGAGAGGCTTAGACT 2220
OY 2221 GGCTCCATTTCCATCTCTATCTCATGCTTTCATCCAGACCCCAACATGAGGG 2280
Db 2221 GGCTCCATTTCCATCTCTATCTCATGCTTTCATCCAGACCCCAACATGAGGG 2280
OY 2281 CCTCAGTATTCGATCATTAATTTCTATTAAGAACAAACAAATTTCCCGCATTTGGCCCA 2340
Db 2281 CCTCAGTATTCGATCATTAATTTCTATTAAGAACAAACAAATTTCCCGCATTTGGCCCA 2340
OY 2341 GTTAATTAAGATTTTCAGATTTTACCTTGAGAAATGCCATGGCTGTATATTCATC 2400
Db 2341 GTTAATTAAGATTTTCAGATTTTACCTTGAGAAATGCCATGGCTGTATATTCATC 2400
OY 2401 TTCAACCTTGCTCCTTCTCTCTGAGAAAGGAAAGTCACTGGATGAGGCTGAGAGACT 2460
Db 2401 TTCAACCTTGCTCCTTCTCTCTGAGAAAGGAAAGTCACTGGATGAGGCTGAGAGACT 2460
OY 2461 AGTGCATGGCTTAAGTCTCTTCATGACTCTGCTTATCTGTTTTCTATTTCTCTCT 2520
Db 2461 AGTGCATGGCTTAAGTCTCTTCATGACTCTGCTTATCTGTTTTCTATTTCTCTCT 2520
OY 2521 TTTCCACCGAAGCTTAATCTCAAGAAAGAGAGAGGAGGCTTGGGCTCTGGCCCA 2580
Db 2521 TTTCCACCGAAGCTTAATCTCAAGAAAGAGAGAGGAGGCTTGGGCTCTGGCCCA 2580
OY 2581 AGAAATATCAAGTCCAGTGAATATCCATGACTACCCCTCTGCTTAACCCCTTTGTG 2640
Db 2581 AGAAATATCAAGTCCAGTGAATATCCATGACTACCCCTCTGCTTAACCCCTTTGTG 2640
OY 2641 ATGGAAGAGCTCCAGGGGCTTTTGTGATGTTACAGGCTTAAGTCAAGTCAAGCA 2700
Db 2641 ATGGAAGAGCTCCAGGGGCTTTTGTGATGTTACAGGCTTAAGTCAAGTCAAGCA 2700
OY 2701 GGGGCAAGAAAGAAAGTAACTTAACCTTAATGCTCTTAATTTGTAATTA 2760
Db 2701 GGGGCAAGAAAGAAAGTAACTTAACCTTAATGCTCTTAATTTGTAATTA 2760
OY 2761 GTTAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
Db 2761 GTTAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
OY 2821 GTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2880
Db 2821 GTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2880
OY 2881 TCAAGTCCGAGCAATTTTTCAAAGTTTAATTTAAATTCATCTATTTGATTTGAT 2940
Db 2881 TCAAGTCCGAGCAATTTTTCAAAGTTTAATTTAAATTCATCTATTTGATTTGAT 2940

QY 2941 GACAGAGAAATGACATGATGAGAGACTAAAGATCTAGCCCAATTTTATTTACTTGG 3000
|||||
Db 2941 GACAGAGAAATGACATGATGAGAGACTAAAGATCTAGCCCAATTTTATTTACTTGG 3000
QY 3001 TTAGAGAGATTTGAACAATTAATCTAAATTTCTTCAAGGTTCAATTTCCCATTAACATATA 3060
|||||
Db 3001 TTAGAGAGATTTGAACAATTAATCTAAATTTCTTCAAGGTTCAATTTCCCATTAACATATA 3060
QY 3061 ATGATAGTCTCATCTTATTTGGGCGCTGAGAGACATATTTCTGTATTTGTATTTAATATC 3120
|||||
Db 3061 ATGATAGTCTCATCTTATTTGGGCGCTGAGAGACATATTTCTGTATTTGTATTTAATATC 3120
QY 3121 ATTGTTATTTATTTATATCATATTTTGGCTTTTAAATGATAGATTTTAAAGATATAG 3180
|||||
Db 3121 ATTGTTATTTATTTATATCATATTTTGGCTTTTAAATGATAGATTTTAAAGATATAG 3180
QY 3181 TAACTGTAAACATTAATGCAAAATGCCGTAGAGACAGTATTAATATATATATAT 3240
|||||
Db 3181 TAACTGTAAACATTAATGCAAAATGCCGTAGAGACAGTATTAATATATATATATAT 3240
QY 3241 TATATTGTAT 3300
|||||
Db 3241 TATATTGTAT 3300
QY 3301 TACAGAAATCTGTATCCCATCTTTCACACACACCCACACATTTTGTCTTTTCCC 3360
|||||
Db 3301 TACAGAAATCTGTATCCCATCTTTCACACACACCCACACATTTTGTCTTTTCCC 3360
QY 3361 ATGCGGTCATCTTAACTTTTGAAGCTT 3388
|||||
Db 3361 ATGCGGTCATCTTAACTTTTGAAGCTT 3388

RESULT 8
AX345239/c
LOCUS AX345239 7201 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 310 from Patent WO200928.
ACCESSION AX345239
VERSION AX345239.1 GI:18493125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Olek A., Piepenbrock C. and Berlin K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 020928-A 310 03-JAN-2002;
Epigenomics AG (DE)
FEATURES
source location/Qualifiers
1..7201
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2131 a 65 c 1603 g 3402 t
ORIGIN

Query Match 67.1% Score 2406; DB 6; Length 7201;
Best Local Similarity 80.6% Pred. No. 0;
Matches 2889; Conservative 0; Mismatches 685; Indels 12; Gaps 6;

QY 183 TCATGGCATGGCGAGGAGTCAAGAGACAGACCTTGCCCTAGTCCCTACCGACGTCAG 242
|||||
Db 5567 TCATTAACATTAACCAAAAATCAAAAACAAACAACTTACTCTCAATATACCTAACCAATACAAA 5508
QY 243 AAAAGTGATAGCCTGGGCGCAGGGCCAGGCGCTGGTGGAGCGTATAGTGAACAGACA 302
|||||
Db 5507 AAAAATACATTAACCTTAACC---GCCAAAACCTTAATTAACGTAATTAATTAACAAAA 5451
QY 303 GGGCTGCTCATTCGAGCCCAAGAGACATTAATTAATTAATTAATTAATTAATTAATTA 362
|||||
Db 5450 AAAGTCTCATTCGAGCCCAAGAGACATTAATTAATTAATTAATTAATTAATTAATTAATTA 5391
QY 363 CAACCCAGCAGACAGGTTCCAGAAAAAGCTCAGGTTGGAACGACGACGACCCGACATC 422
|||||
Db 5390 CAACCCAGCAGACAAATTCAAAAAATTCAGTTTAAACCAATACCCGACGAC 5331
QY 423 ACAGACACCACTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 482
|||||
Db 5330 AACCAACACCAATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5271
QY 483 CTGCGCCATGCTCAAGTGTAGTGGCGCTTCTGATGCTGCTGACATCTTATAGAA 542
|||||
Db 5270 CTACCCATATCTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5211
QY 543 GGAACACTGAAGAAAGAACTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 602
|||||
Db 5210 AAACACTGAAGAAAGAACTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 5151
QY 603 CTAAATTAATTTGTACATGAATGAATCAAGAGAGTTTAAACCTTTGGACTAAATG 662
|||||
Db 5150 CTAAATTAATTTGTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5091
QY 663 TGTGAATCCTTTTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 722
|||||
Db 5090 TATTAATCCTTTTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 5031
QY 723 TTGAGACTAAGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 782
|||||
Db 5030 TTAAACACTAAGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4971
QY 783 TGAACCTCAC-TTTGTAAATCTTGACAGGGGCAATCCAAATATCTGCACAGAGATATGT 841
|||||
Db 4970 TAACTCACTTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4916
QY 842 TAACAGCTGTAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 901
|||||
Db 4915 TTAAACACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4856
QY 902 TTCTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 961
|||||
Db 4855 TTCTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4797
QY 962 GCCATTTTAAAGCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1021
|||||
Db 4796 ACCATTTTAAAGCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4737
QY 1022 TTGAGACTGTAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1081
|||||
Db 4736 TTAAACACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4677
QY 4676 TTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4617
Db 1142 GGGCTGATACAGTTCACGACGCTCAACCTTTTGTAGGCTCAAGGATTTCTCCACCTCA 1201
|||||
Db 4616 GACGTAATACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4557
QY 1202 GCCCCCAAGTATTTGGGAGCAGACGATGATGATGATGATGATGATGATGATGATGATGAT 1261
|||||
Db 4556 ACCCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 4497
QY 1262 TTGTAGAGATGAGATCTCATTAATTTGTCAAGGCTGTCTTGAATTTCTTGCGCTCAGGT 1321

[illegible]

Dd	3416	TTTATTAACATTTCTCATAATTTACCTTAAAAAATACCATTGCACCTATATATTCACATCT	3357
Qy	2402	TCACCTTGTCCCTTCCTCCTAGAAAAGAGAAAGTCAGTTGGATGCCCTCTGAGAGACTA	2461
Dd	3356	TCACCTTATCCCTTCCTCCTAAAAAATAAATCAATTAATACCTCTAAAAAATCA	3297
Qy	2482	GTGANTGGCTTAACCTGTCCCTGCATCCTCCCTTATCTGTTCATTTTCCTCCTT	2521
Dd	3296	ATACATTAACCTTAACCTATACCTTCCTCAATCTCAATCTATCTATTTTCTATTTTCCTCCTT	3237
Qy	2522	TTCCACGGAAGCTATATATCTCAAGAAAAGCAGGACCTGGCCTGGAGGCTCTGGCCTTA	2581
Dd	3236	TTCCACGCGAATCTATATATCTCAAAAAAACAACACTAAGCTTAACCTTAACCTCAACTAA	3177
Qy	2582	GAAATATCAAGTCCAGTGAAGAAATCCCAATGACTGACCCCTCCTCTATCCCTTTGTGA	2641
Dd	3176	AAAAATCAAAATCCAAATAAAAAACCCATTAACCTACCCCTCCTACTTAACCCCTTATATA	3117
Qy	2642	TGGAAAGCTCCCAAGGGGTTGCTTTTGTGATGTACCAAGGCTTAACTCAGATCCAG	2701
Dd	3116	TAAAAAAATCCCAAAATTTACTTTTTTATATTTACCAAACTCAACATCAATCACAA	3057
Qy	2702	GGGCAGAAAAGGAAAGTAACCTAAGCTATATCGCTTTATTTGTAATTTATTTAGTAG	2761
Dd	3056	AAACAAAAAATAAATAAATAAATTAACCTTAACCTAATCTACTTTAATTTATTAATTAATA	2997
Qy	2762	TTAATTAAGTATGTATGTACATGTGTAAACAGACAAATGTATTTTTCACAGCTGCTG	2821
Dd	2996	TTAATTTCTATATATATATACATATATAACAACAAATATATTTTTCACAACTACTA	2937
Qy	2822	TGGATGGATTAATGCCATTTTGGATTAAGAATGCTGTTAAGACACACAGCCAGTTCCT	2881
Dd	2936	TAAATTAATTTTACCATTTTAAATTAATAAATACTATTAATAAACACAAACCAATTTCT	2877
Qy	2882	CAAGCCGTACCAATTTTTCAAAGTAAATTAATAATTAACCTCAATTTGATGTAGT	2941
Dd	2876	CAATTCGTACCAATTTTTCAAATTAATTAATTTAATTTAATTTAATTTAATTAATTA	2817
Qy	2942	ACAGAGAAATGAGCATGGATAGAGACTAAGACTAGGCCAAATTTTATATTTACTTGT	3001
Dd	2816	ACAAAAAATAAATCAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	2757
Qy	3002	TAGAGATTTTGAAACAATTAATTAATTTCTTAAGGTCAATTTTCCCATTAACATAA	3061
Dd	2756	TAAAAAATTTTAAACAATTAATTAATTTCTTCAAAATTCATTTCCCATTAACATAA	2697
Qy	3062	TGAATGCTCATCTAATTTGGGCGCGAGAACATTAATTAATTTGTAATTAATTA	3121
Dd	2696	TAAATTAACCTCACTTTTAAAAACCCCTTAATAAACAATTAATTAATTAATTAATTA	2637
Qy	3122	TTGTTATTTATTTATATATATTTTGTCTTTTAAATGATTAAGATTTTAAAGTATATGT	3181
Dd	2636	TTATTTATTTATTTATATATATTTTACTTTTAAATTAATAAATAAATAAATAAATAA	2577
Qy	3182	AAACTGTAAAAATTAATGCAAAATGCGGTAAAGACAGTGTATATATATATATATTT	3241
Dd	2576	AAACTATTAATAAATTAATAAATACCAAAATACGCTAAAAAACAATATATATATATATAT	2517
Qy	3242	ATATTTGATATATATAGCTAGCTGTTTTTCCGTGTGTATTTCTCCTTTAAATGCTT	3301
Dd	2516	ATATTTATTTATATATATATCAACCTATTTTTCCTATTTTATATTTCTCCTTTAAATFAC	2457
Qy	3302	ACAGAAATCTATATCCCATTTTCACACACACCCACAATTTCTGCTCTTTTCCCA	3361
Dd	2456	TCAAAAATCTATATCCCATTTTCACACACACCCACAACATTTCTACTTCTTTTCCCA	2397
Qy	3362	TGCCG-GTGATGCTAAGCTTGAAGGCTCAGCTTTTCCCTCCTCAATCTTTCCTGCG	3420
Dd	2396	TACGGAATCATTAAGCTTAAAAAGCTCAACCTTTCCTCCTCAATCTTTCCTCAAC	2337
Qy	3421	ACCTCTGATATGCTTTTGAATTCATGTTAAGAATCCCTTAGCTGCTATCACATGTGG	3480
Dd	2336	ACCTCTATATATCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2277

Db 3065 TTTAAAGTGTGATTTCTTTTAAATATTTTTCAGAGAAAAGGAAATAATTAATATA 3124
 Oy 1681 TTAAAGGTGAATACAGGCTACATACCTTCTCCAGATATAGAGCTCTCTCTTT 1740
 Db 3125 TTACGGTGAATATAGGTTATATTTTGTATTTTGTAGATATAGTATTTCTTTT 3184
 Oy 1741 CTTCCTTAGAGCTCAAGTGCAGAGACACTCTGTGATTTAGCTGTGTACTGACAA 1800
 Db 3185 TTGCTTTAGATGTGAAGTGAAGGATTTTGTGATTTAGCGTGTATATGATA 3244
 Oy 1801 AATGTATTTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGATTTG 1860
 Db 3245 AAGGTATTTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGATTTG 3304
 Oy 1861 TGATGGAGACACAAACATTTGCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920
 Db 3305 TGATGGAGATATATTAATTTATTTTGTATTTTGTATTTTGTATTTTGTATTTT 3364
 Oy 1921 ATGTGCAATTCAGTGGAGATGATCTGACAGACACCCATGAAAAGATCAACAAT 1980
 Db 3365 ATGTGCAATTCAGTGGAGATGATCTGACAGACACCCATGAAAAGATCAACAAT 3424
 Oy 1981 TCCACCAAGGACCTATTTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGAT 2040
 Db 3425 TTTATTTAGGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 3484
 Oy 2041 TTTATTTAGGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2100
 Db 3485 TTTATTTAGGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 3544
 Oy 2101 CACTGCATTTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGATTTG 2160
 Db 3545 TTTATTTAGGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 3604
 Oy 2161 GTAAAGAGGCTGATTTAGGAGATTTAGGAGATTTAGGAGATTTAGGAGATTTAGG 2220
 Db 3605 GTAAAGAGGCTGATTTAGGAGATTTAGGAGATTTAGGAGATTTAGGAGATTTAGG 3664
 Oy 2221 GGTCCATTTCCATCTATTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGAT 2280
 Db 3665 GGTCCATTTCCATCTATTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGAT 3724
 Oy 2281 CCTCAGTATTCATCTATTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGAT 2340
 Db 3725 TTTATTTAGGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 3784
 Oy 2341 GTATTTAGGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2400
 Db 3785 GTATTTAGGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 3844
 Oy 2401 TTTACCTTTGCTCCTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGAT 2460
 Db 3845 TTTATTTTGTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 3904
 Oy 2461 AGTGCATTTGCTCCTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGAT 2520
 Db 3905 AGTGCATTTGCTCCTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGAT 3964
 Oy 2521 TTTCCACCGAGCTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2580
 Db 3965 TTTTTCGAGGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 4024
 Oy 2581 AGAATATCATCTCAGTGAATATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2640
 Db 4025 AGAATATCATCTCAGTGAATATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 4084
 Oy 2641 ATGGAGAGCTCCAGGCTTTGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2700
 Db 4085 ATGGAGAGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 4144
 Oy 2701 GGGGAGAGAGAGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2760

Db 4145 GGGGAGAGAGAGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 4204
 Oy 2761 GTTAATTTACGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2820
 Db 4205 GTTAATTTACGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 4264
 Oy 2821 GTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2880
 Db 4265 GTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 4324
 Oy 2881 TCAATTCCTGACAAATTTTCAAAAGTTAAATTTAAATTCATTTGATTTGATTTGATTT 2940
 Db 4325 TCAATTCCTGACAAATTTTCAAAAGTTAAATTTAAATTCATTTGATTTGATTTGATTT 4384
 Oy 2941 GACAGAGAAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3000
 Db 4385 GACAGAGAAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4444
 Oy 3001 TTAGAGATTTTTCACAAATTTTCTCAAGTTCAAGTTTCCATTTAATCTATA 3060
 Db 4445 TTAGAGATTTTTCACAAATTTTCTCAAGTTTCCATTTAATCTATA 4504
 Oy 3061 ATGAATGCTCATTTATTTAGGAGCTGAGAGACATTTATTTGATTTGATTTGATTTGAT 3120
 Db 4505 ATGAATGCTCATTTATTTAGGAGCTGAGAGACATTTATTTGATTTGATTTGATTTGAT 4564
 Oy 3121 ATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 3180
 Db 4565 ATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4624
 Oy 3181 TAAATGTAATTAATTTAAATTTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 3240
 Db 4625 TAAATGTAATTAATTTAAATTTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 4684
 Oy 3241 TAAATGTAATTAATTTAAATTTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 3300
 Db 4685 TAAATGTAATTAATTTAAATTTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 4744
 Oy 3301 TAAATGTAATTAATTTAAATTTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 3360
 Db 4745 TAAATGTAATTAATTTAAATTTGAGAGATTTGATTTGATTTGATTTGATTTGATTTGAT 4804
 Oy 3361 ATG-CCGTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3419
 Db 4805 ATG-CCGTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 4864
 Oy 3420 CACTGCATTTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGATTTGAT 3479
 Db 4865 CACTGCATTTTCTCAGCTGCTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 4924
 Oy 3480 GCATTTTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3539
 Db 4925 GCATTTTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 4984
 Oy 3540 TCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3586
 Db 4985 TCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 5031

RESULT 10
 AF262300
 LOCUS AF262300 1310 bp mRNA linear PRI 26-JUN-2002
 DEFINITION Homo sapiens clone 2 CC chemokine receptor 3 (CCR3) mRNA, partial -
 cds.
 ACCESSION AF262300
 VERSION AF262300.1 GI:19171642
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 1310)
 Vlijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and


```
misc.feature
1. .436
/chromosome="3"
/map="3p21"
/clone="7"
/cell_type="primary eosinophil"
1. .436
```

CC chemokine receptor 3-like; contains exon 1, exon 3, and intron 3 of the CCR3 gene; alternatively spliced"

Query Match	10.0%;	Score 358.6;	DB 9;	Length 436;
Best Local Similarity	98.9%;	Pred. No. 1.1e-63;		
Matches 361;	Conservative	0;	Mismatches 4;	Indels 0;
			Gaps	0

Qy	2809	TTTCACAGCTGCTGTGGATTGATGCCAATTTGGAATAAGCATGCTGTTAAGACACAC	2868
Db	72	TTTTACAGCTGCTGTGGATTGATGCCAATTTGGAATAAGATGCTGTTAAGACACAC	131

Qy 2869 AAGCCAGGTTCCCTCAAGTCGGTAGCAAAATTTTCAAAAAGTTAAATTTAAAAATCAGTACA 2928
 |||||
 Db 132 AAGCCAGGTTCCCTCAAGCGCGTAGCAAAATTTTCAAAAAGTTAAATTTAAAAATCAGTACA 191

Qy	2229	TTTGGATCTAGTGACAGGAGAAATGACATGGATAGAGCTAAAGATCTAGCCCAATTTT	2988
Db	192	TTTGGATCTAGTGACAGGAGAAATGACATGGATAGAGCTAAAGATCTAGCCCAATTTT	251

QY 2989 TATATTACTGTTAGAGCATTTTGACAAATTTACTAAATTTCTTCAAGGTTCAATTTCC 3048
|||||
Db 252 TATATTACTGTTAGAGCATTTTGACAAATTTACTAAATTTCTTCAAGGTTCAATTTCC 311
|||||

QY 3049 CCATTACCTATAATGCAATGCTCATCATATTATGGGCCCCGGAGAAGCATTAATTACTTGTAA 3108
|||||
db 312 CCATTACCTATAATGCAATGCTCATCATATTATGGGCCCCGGAGAAGCATTAATTACTTGTAA 371

Dh 372 ATTTCTAATAATCATTTCCTTAATTAATACACTAAATTTTCCCTTTTTTAAATGCAAGCATTTT 431

OY 3109 ATTGAATAATCATCTGTAAATTATTAATTACATATTTCCTTTTAAATGCAAGCATTTT 3168

QY	3169	TPAAG	3173
Ob	423	TPAAG	426

RESULT 12
BD006761

DEFINITION	Chemokine receptors 88-2B [CKR-3] and 88C and antibodies thereof.
ACCESSION	BD006761
VERSION	BD006761.1 GI:18635132

SOURCE ORGANISM	REFERENCE
unidentified.	1
unidentified	2
unclassified.	3
unclassified.	4

REFERENCE
1 (bases 1 to 1913)
AUTHORS
Gary, P.W., Shelcart, V.L. and Rayport, C.J.
TITLE
Chemokine receptors 88-28 [CCR-3] and 88C and antibodies thereof
JOURNAL
Database: JP 2001020089-23 06-Feb-2001.

COMMENT
ICOS CORP
OS Unidentified
PN JP 2001029089-A/2
de-mps 2003
nd

PF 16-MAY-2000 JP 2000143832 08/661393 PI
PR 20-DEC-1995 US 08/575967,07-JUN-1996 US
PATRICK W GARY,VICWIKI L SHEICART,CARROLL J RAYPORT PC

C12N5/10, PC C12N5/10, C12N15/02, C12P21/02, C12P21/08, C12Q1/68, G01N33/15, PC G01N33/50,

A61P7/02, PC A61P17/06, PC A61P19/02, A61P29/00, A61P31/12, (C12P21/02, C12R1:91), C12N5/00, PC C12N5/00,

7
C
H
N
C
C
C
N
H
C
C

CC	Strandedness: Single;	
CC	Topology: Linear;	
FH	Key	Location/Qualifiers
FT	CDS	362..1426.

```
source      1. 1915
            /organism="unidentified"
            /db_xref="taxon:32644"
```

Query Match	9.68;	Score 344.2;	DB 6;	Length 1915;
Best Local Similarity	98.98;	Pred. No. 1.9e-66;		

3227 ATATAATGATTATTATTTGTTATCATTTATCTAGCCGTGTTTTCCGTGTGTAATTC 3286

3287 TTCCTTAAATGCTTACAGAAATCTGTATCCCATTTCTTCACCCACGCCACACACATTTT 3346

DZ 01 ATTCCATTTTAAACCATCAGGTAAGAATTCTTCCTCGTG
QY 3347 CTGGTCTTTTTCCCATTGCC-GGTCAATGCATACTTTGAAGCTTCAGCTCTTTCCCTCTGC 3405

DD 121 CAGGTCCTTTCCTGCGACCTGATATGCCCTTTGAATTTCATGTTAAAGAATCCCTAGGC 3465
 QY 3406 AATTCCTTCTCTCTGCGACCTGATATGCCCTTTGAATTTCATGTTAAAGAATCCCTAGGC 3465

DB 181 AATTCCTTTTCCGCGCACCCTGATGATATGCCCTTTTGAATTCATGTTAAGAAATCCCTAGGC 240

QY 3466 TGCCTATCACATGTGCCATCTTTGTTGAGTACATGAATAAATCAACTGGTGTGTTTACGA 3525

DB 241 TGCATCACATGAGGCACCTTTGTTGAGTACATGAATAAATCAACIGGTGTTTACGA 300

QY 3526 AGGATGATTATGCTTCATTGCTGGGATGTATTTTCTTCTCTATCACAGGGAGAAGTGA 3585

Db	301	AGGATGATTATGCTTCATTGAGGATGTATTTTCTTCCTATACACAGGGAAGTGA	360
QY	3586	A	3586

RESULT 13

LOCUS	AC025177	112967 bp	DNA	linear	PRI 22-MAY-2002
DEFINITION	Homo sapiens chromosome 5 clone CTD-213I18, complete sequence.				
ACCESSION	AC025177				

VIRGILIO
KEYWORDS
SOURCE
ORGANISM

01.12.10000
HTG.
Homo sapiens.
Homo sapiens
Homo sapiens

[illegible]

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 112967)
 REFERENCE

TITLE Direct Submission
JOURNAL Submitted (07-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

AUTHORS
TITLE
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (22-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL

COMMENT
On May 22, 2002 this sequence version replaced gi:15290360.
Draft sequence produced by DOE Joint Genome Institute
www.jgi.doe.gov

FINISHING COMPLETED AT STANFORD HUMAN GENOME CENTER


```
repeat_region /rpt_family="ERV.L"
806. .1097
/rpt_family="7.SLRNA"
repeat_region 1100. .1391
/rpt_family="Alu"
repeat_region 1399. .1447
/rpt_family="ERV.L"
repeat_region 1534. .1825
/rpt_family="Alu"
repeat_region 1826. .2139
/rpt_family="Alu"
repeat_region 2291. .2424
/rpt_family="ERV.L"
repeat_region 2561. .2850
/rpt_family="Alu"
repeat_region 2863. .2993
/rpt_family="Alu"
misc_feature 3219. .5173
/note="CpG_island (%GC=78.2, o/e=0.80, #CpGs=188)"
repeat_region 3443. .4209
/rpt_family="SVA"
repeat_region 4277. .4789
/rpt_family="SVA"
repeat_region 4983. .5408
/rpt_family="SVA"
repeat_region 5468. .5603
/rpt_family="Alu"
repeat_region 5604. .5901
/rpt_family="Alu"
repeat_region 5910. .6190
/rpt_family="Alu"
repeat_region 6191. .6348
/rpt_family="Alu"
repeat_region 6482. .6773
/rpt_family="Alu"
repeat_region 6829. .7001
/rpt_family="Alu"
repeat_region 7160. .7329
/rpt_family="Alu"
repeat_region 7367. .7471
/rpt_family="ERV.L"
repeat_region 7484. .7561
/rpt_family="Alu"
repeat_region 7562. .7836
/rpt_family="Alu"
repeat_region 7857. .8003
/rpt_family="Alu"
repeat_region 8084. .8323
/rpt_family="Alu"
repeat_region 8331. .8628
/rpt_family="Alu"
repeat_region 8629. .8705
/rpt_family="ERV.L"
repeat_region 8935. .9342
/rpt_family="MALR"
repeat_region 9468. .9577
/rpt_family="Alu"
repeat_region 9673. .9978
/rpt_family="Alu"
repeat_region 9979. .10278
/rpt_family="Alu"
repeat_region 10429. .10738
/rpt_family="Alu"
repeat_region 11243. .11807
/rpt_family="MALR"
repeat_region 11808. .12099
/rpt_family="Alu"
repeat_region 12100. .12164
/rpt_family="MALR"
repeat_region 12462. .12524
/rpt_family="t2"
misc_feature 12479. .13351
/note="CpG_island (%GC=77.5, o/e=0.80, #CpGs=108)"
```

misc_feature	13117..13207	/note="similar to	EST AI702629 (NID:g4990529)	we06a07.x1"
misc_feature	13117..13207	/note="similar to	EST BE676284 (NID:g10036825)"	
misc_feature	13117..13207	/note="similar to	EST BE676622 (NID:g10037163)"	
misc_feature	13118..13207	/note="similar to	EST AA900454 (NID:g4232946)"	
misc_feature	13118..13207	/note="similar to	EST BF512598 (NID:g11597777)"	
misc_feature	13163..13207	/note="similar to	EST BF582271 (NID:g11655983)"	
repeat_region	14343..14554	/fpl_family="MIR"		
repeat_region	15323..15417	/fpl_family="L2"		
repeat_region	15528..15798	/fpl_family="L2"		
repeat_region	16318..16530	/fpl_family="MIR"		
repeat_region	16655..16706	/fpl_family="MIR"		
repeat_region	16718..16827	/fpl_family="L2"		
repeat_region	16838..17148	/fpl_family="Alu"		
repeat_region	17283..17619			

Query Match	6.1%	Score 218.2	DB: 9	Length 131329
Best Local Similarity	74.3%	Pred. No. 2.7e-38		
Matches 289	Conservative 0	Mismatches 98	Indels 2	Gaps 1
QY 1012	TTACCTTGATTTGAGACATGGGATGACAGAGTGCAAAACCATATCAGGGTTTTTAATTTTTTAA	1071		
Db 23473	TTAACAATATTTATATGTAATATATATATTTTAACTATTTTAAATATATATATATATAT	23532		
QY 1072	TTTTTAATTTATTTATTTATTTATTTATTTTGTGAGATGGAGTCTGG--CTGTGCCCAAGG	1129		
Db 23533	TATTTATTTATTTATTTATTTATTTATTTATTTTGTGACAGAGAGCTGCTGTGCACCCAGG	23592		
QY 1130	CTGGAGTGCAGGGGGGTATATCATCAGTTACAGTCCACCCATCAGCTCTGAGGATCAGGAT	1189		
Db 23593	CTGGAGTGCAGAGGTGTGTATCTCAGCTTACTCTACAGCTTCCACCTCTGTGGTTCAAGTATC	23652		
QY 1190	TCTCCACCTCAGCCCCCAAGTAGTTGGGACACAGCATATGCGCCACATGCTGAGCTA	1249		
Db 23653	TCTCTGCTGCTCAGCTCCCAAGTAGTCTCGATTTACAGCATATGACACACCATGCTGAGCTA	23712		
QY 1250	ATTCTCTATTTTTTTGTGAGATATAGATCTCATTTATTTGTCACAGGCGTCTGTAATTC	1309		
Db 23713	ATTTTGTATCTTTTAGTATGATATGGGGTTTCCCATGTTGGCCAGGCTGTGTAACCTT	23772		
QY 1310	CTGGGCTCAGGTGAGCCTCCACCACTCGGGCCTCCCAAGTACTGGGATTAACGCATGAGC	1369		
Db 23773	CTGACCTCAGGTGATCCACACTCCTCAGGCTCCCAAGAGTGTGGATTAACAGCATGATTC	23832		
QY 1370	CAAGGTCCCTCGCCCATATGAGATTTTCT	1398		
Db 23833	CACGCTGCCACAGCCCTCTCTATCTTCT	23861		

RESULT 15
HS00024/C
LOCUS
DEFINITION

HS00024 157435 bp DNA linear PRI 17-MAY-2000
 Human DNA sequence from clone RPI-50024 on chromosome 1p35.1-35.3. Contains the 3' end of the gene for a novel protein similar to C. elegans K07B1.7 (TT:001866), the gene for a novel protein (translation of cDNA NR2M2001100 (Em:AK001211)), the SN gene for stratifin (14-3-3 protein sigma), the gene for a novel protein with DHC zinc finger domain, the gene for a novel protein (translation of cDNA K010271 (Em:AK000484)) and the gene for B120 (Clorf4) (A12D DNA binding domain containing protein). Contains ESTs, STSs, GSSs and six putative CpG islands, complete sequence.

